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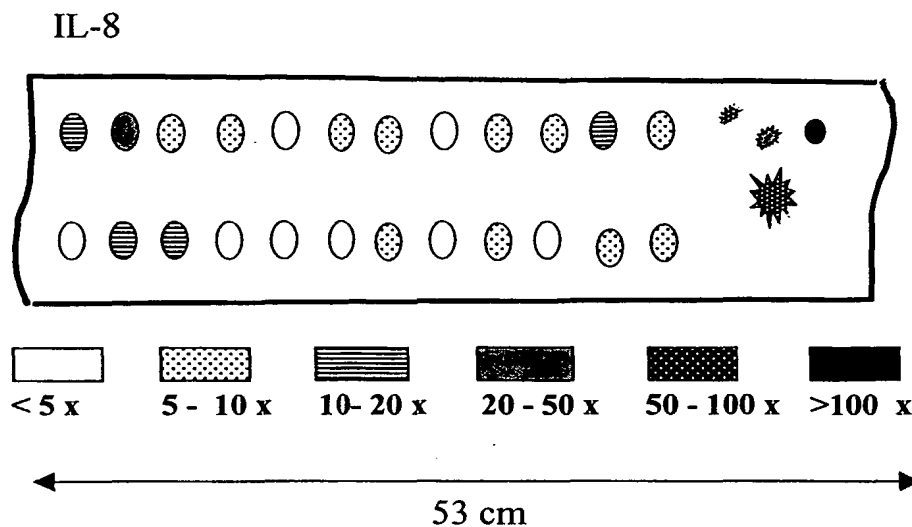
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(54) Title: BIOMARKER PANEL FOR COLORECTAL CANCER



(57) Abstract: A panel of biomarkers has been identified for analysis of colorectal cancer. The panel, originally identified using a mouse colon cancer model, has been used to assess changes in human tissue from surgical and biopsy samples against a normal human control panel of biomarkers. The panel may be used for providing a cost effective, rapid, noninvasive procedure for risk assessment, early diagnosis, establishing prognosis, monitoring patient treatment, detecting relapse, and for the discovery of therapeutic intervention of colorectal cancer.



WO 2005/010486 A2

BIOMARKER PANEL FOR COLORECTAL CANCER**Reference to Related Applications**

5 This application claims priority to U.S. Provisional Patent Application
60/488,660 entitled Molecular Marker Panel for Determination of Colorectal
Cancer, by Nancy M. Lee et al., filed July 18, 2003 (Attorney Docket CPMC-
01000US0); and U.S. Patent Application 10/690,880 entitled Biomarker
Panel for Colorectal Cancer, by Nancy M. Lee et al., filed October 22, 2003
10 (Attorney Docket CPMC-01000US1), both of which are incorporated herein
by reference.

Background

 The field of art of this disclosure concerns biomarkers for colorectal
cancer (CRC). These biomarkers are useful for risk assessment, early
15 detection, establishing prognosis, evaluation of intervention, recurrence of
CRC, and discovery of therapeutic intervention, and methods of use thereof.

 In the field of medicine, clinical procedures providing for the risk
assessment and early detection of CRC have been long sought. Currently,
CRC is the second leading cause of cancer-related deaths in the Western
20 world. One picture that has clearly emerged through decades of research
into CRC is that early detection is critical to enhanced survival rates.

 The currently accepted methods for CRC screening include the fecal
occult blood test (FOBT), x-ray using double contrast between barium
enema and air (DCBE), sigmoidoscopy, and colonoscopy. Sigmoidoscopy is
25 an invasive procedure that visually examines the lower third of the colon
using a lighted, flexible endoscope, while a related method, colonoscopy, is
a procedure that examines the entire colon. In both cases, biopsy samples
can be taken during the procedure.

 Concerning the accepted methods for screening, none clearly
30 possess what is desired in a screening examination for CRC. While FOBT is

rapid, it is a very general, and therefore a very non-specific screening method for CRC. Though DCBE has proven useful in specifically imaging abnormalities in the colon, the drawbacks of the DCBE method include: 1.) Patient discomfort in preparation of and during the examination, creating reluctance for compliance of DCBE as a screening method. 2.) Exposure of a patient to x-ray radiation, limiting DCBE in terms of frequency of use as a screening method. 3.) Research indicating that DCBE is more effective in detecting larger growths, which contraindicates its use for early detection. 4.) Biopsy samples cannot be taken during the procedure. 5.) Due to the cost involved, not all insurance providers pay for DCBE screening exams.

Though sigmoidoscopy has gained favor from many physicians, the drawbacks of this method include: 1.) Patient discomfort in preparation of and during the examination, creating reluctance for compliance of sigmoidoscopy as a screening method. 2.) Due to the cost involved, not all insurance providers pay for sigmoidoscopy screening exams. 3.) Since only the lower third of the colon is inspected, there is a suggestion by studies that many significant lesions are in the proximal end of the colon, rendering sigmoidoscopy inadequate. Though colonoscopy addresses the issue of complete inspection of the colon, the drawbacks of colonoscopy as a screening method include: 1.) Creating even more patient discomfort than sigmoidoscopy, therefore generally requiring sedation, and thereby exacerbating the issue with patient compliance. 2.) Due to the cost involved, not all insurance providers pay for colonoscopy screening exams. 3.) There are risks of colonoscopy that include bleeding, and puncture of the lining of the colon.

Emerging spectroscopic technologies, such as magnetic resonance imaging and tomographic imaging each have drawbacks that are drawn from the list of drawbacks for the currently accepted screening methodologies.

Accordingly, there is a need in the art for approaches that have value in early detection and treatment of CRC that are cost effective, rapid, and

minimally or noninvasive. Additional utility would be realized from an approach that would also serve as the basis for establishing prognosis, monitoring patient treatment, and detecting relapse, as well as the discovery of therapeutic intervention of CRC.

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Brief Description of Figures

FIG 1 is a summary of the sequence listings.

FIGS 2A-2C show data that illustrate a panel of biomarkers for samples taken from adenomous polyps, and suspect tissues vs. normal controls. FIGS 2A-2B are tables that compare the results of model studies done in mouse (2A) for a selection of members of the set of 22 biomarkers listed in the sequence listings with the comparable selection in of biomarkers for human subjects (2B). FIG 2c shows the multivariate analysis for 9 markers for 78 biopsies taken from 12 normal patients and 63 biopsies taken from 6 patients with CRC.

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FIGS 3B-3C show expression levels for representative biomarkers, IL-8 (3A), CXCR-2 (3B), and COX-2 (3c) for a series of samples taken from a human subject comparing a histologically identified cancerous lesion, a polyp, and an adjacent non-cancerous tissue vs. a normal control.

FIGS 4A-4C show the results of multiple analysis across a 53 cm distance of a colon for a patient with CRC: 4A shows expression levels for IL-8; 4B shows expression levels for COX-2; and 4c shows expression levels for CXCR-2.

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Detailed Description

Still another sought after approach apart from currently accepted methods for screening for CRC, has been the search for biomarkers that have value in detection and treatment of CRC. For more than four decades, since the discovery of alpha-fetoprotein (AFP) and carcinogenic embryonic antigen (CEA), the search for biomarkers for cancer detection and treatment in general has been in a state of evolution. Biomarkers for cancer have five potential uses in the management of patient care. Ideally, they would be

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used for risk assessment, for early diagnosis, for establishing prognosis, for monitoring treatment, and for detecting relapse. Additionally, such markers could play a valuable role in developing therapeutic interventions.

5 It is further advantageous for the sampling methods used in conjunction with biomarker analysis to be minimally invasive or non-invasive. Examples of such sampling methods include serum, stool, swabs, and the like. Non-invasive and minimally invasive methods increase patient compliance, and generally reduce cost.

10 Clinically, the two criteria that are important for assessing the effectiveness of biomarkers are selectivity and sensitivity. Selectivity of a biomarker defined clinically refers to percentage of patients correctly diagnosed. Sensitivity of a biomarker in a clinical context is defined as the probability that the disease is detected at a curable stage. Ideally, biomarkers would have 100% clinical selectivity and 100% clinical sensitivity.
15 To date, no single biomarker has been identified that has an acceptably high degree of selectivity and sensitivity required to be effective in for the broad range of needs in patient care management. However, from the clinical perspective, single serum biomarkers, such as AFP and CEA have proven to provide value in some aspects of patient care management.

20 For example, elevated serum levels of CEA were first discovered in 1965 in patients with adenocarcinoma of the colon. Elevated levels can be found in a variety of benign and malignant conditions other than colon cancer. Additionally, the production of CEA by early localized tumors of the colon is in the normal range. Therefore CEA lacks both the sensitivity and selectivity required to be of value for risk assessment or early diagnosis.
25 Further, elevated levels of CEA correlate poorly with colon tumor differentiation and stage, rendering CEA as a biomarker for prognosis of colon cancer of limited value. The two areas for which CEA has proven helpful clinically in managing patient care are in evaluating the effectiveness
30 of treatment, and for detecting relapse. Illustrative of this, numerous studies

have found that there is high correlation between elevated serum levels of CEA preceding clinical detection of recurrence of colon cancer. This has proven to be of value in managing the care of high-risk patents with second-look surgical procedures based on rising levels of CEA.

5 Currently, investigations across numerous areas of oncology research, including CRC, ovarian, breast, and head and neck, are finding increased sensitivity and selectivity in panels of markers. It is now generally held that many mutations must take place before normal cell processes are altered, resulting in a disease, such as cancer. Still, given the complexity of
10 biological systems, discovery of panels useful in providing value in patient care management for CRC is in the nascent stage.

 To date, a greater understanding of the biology of CRC has been gained through the research on adenomous polyposis coli (APC), p53, and Ki-ras genes, as well as the corresponding proteins, and related pathways
15 involved in the regulation thereof. However, there is a distinct difference between research on a specific a gene, its expression, protein product, and regulation, and understanding what genes are critical to include in a panel used to for the analysis of CRC that is useful in the management of patient care for the disease. To date, panels that have been suggested for CRC are
20 comprised of specific point mutations of APC, p53, and Ki-ras, as well as BAT-26, which is a gene that is a microstatelite instability marker.

 What is disclosed herein is based on studies conducted in mouse multiple intestinal neoplasia (MIN) model, in which expressions levels of genes were screened in adenomous polyps. In the mouse MIN subjects, a
25 chemically induced mutation of the APC gene is effected. The normal control is defined by littermates for which there was no aberration of the APC gene, and are therefore designated wildtype. From studies based on the mouse MIN model, candidate genes were selected for studying human subjects. From these human subject studies, a panel of biomarkers is disclosed
30 herein. Further, what is disclosed are methods for measuring gene and

protein expression levels based on the panel. Additionally, another aspect of what is disclosed are kits which provide the reagents and instructions for measuring gene and protein expression levels based on the panel. The panel, methods and kits are useful in the management of patient care for CRC. Additionally, the panel, methods, and kits are believed useful as the basis for discovery of therapeutic interventions for CRC.

FIG 1 is a table that gives an overview of the sequence listing for the disclosed biomarkers. The combination of biomarkers disclosed forms the basis for monitoring CRC with enhanced selectivity and sensitivity, and therefore providing enhanced management of patient care for CRC. It is to be understood that fragments and variants of the biomarkers described in the sequence listings are also useful biomarkers in a panel used for the analysis of CRC. What is meant by fragment is any incomplete or isolated portion of a polynucleotide or polypeptide in the sequence listing. It is recognized that almost daily, new discoveries are announced for gene variants, particularly for those genes under intense study, such as genes implicated in diseases like cancer. Therefore, the sequence listings given are exemplary of what is now reported for a gene, but it recognized that for the purpose of an analytical methodology, variants of the gene, and their fragments are also included.

One embodiment of what is disclosed is a panel of biomarkers with the selectivity and sensitivity required for managing patient care for CRC. In Table 1, entries 1-22 are the polynucleotide coding sequences for a panel of biomarkers, and include the name and abbreviation of the gene. Entries 23-44 in Table 1 are the protein, or polypeptide, amino acid sequences that correspond to the coding sequences for entries 1-22. A biomarker, as defined by the National Institutes of Health (NIH) is a molecular indicator of a specific biological property; a biochemical feature or facet that can be used to measure the progress of disease or the effects of treatment. A panel of biomarkers is a selection of biomarkers. Biomarkers may be from a variety of

classes of molecules. As previously mentioned, there is still a need for biomarkers for CRC having the selectivity and sensitivity required to be effective for all aspects of patient care management. Therefore, the selection of an effective set of biomarkers is differentiating in providing the basis for effective determination of CRC.

In another embodiment of this disclosure, expression levels of polynucleotides for the biomarkers indicated in SEQ ID NOs 1-22, are used in the determination of CRC. Such analysis of polynucleotide expression levels is frequently referred to in the art as gene expression profiling. In gene expression profiling, levels of mRNA in a sample are measured as a leading indicator of a biological state, in this case, as an indicator of CRC. One of the most common methods for analyzing gene expression profiling is to create multiple copies from mRNA in a biological sample using a process known as reverse transcription. In the process of reverse transcription, the mRNA from the sample is used to create copies of the corresponding DNA sequence from which the mRNA was originally transcribed. In the reverse transcription amplification process, copies of DNA are created without the regulatory regions in the gene known as introns. These multiple copies made from mRNA are therefore referred to as copy DNA, or cDNA. Entries 45-88 are the sets of primers used in the reverse transcription process for each gene listed in entries 1-22.

Since the reverse transcription procedure amplifies copies of cDNA proportional to the original level of mRNA in a sample, it has become a standard method that allows the analysis of even low levels of mRNA present in a biological sample. Genes may either be up regulated or down regulated in any particular biological state, and hence mRNA levels shift accordingly.

In still another embodiment of this disclosure, expression levels of proteins listed in SEQ ID NOs 23-44, which correspond to the genes indicated in SEQ ID NOs 1-22, are disclosed. The term "polypeptide" or

“polypeptides” is used interchangeably with the term “protein” or “proteins” herein. As discussed previously, proteins have been long investigated for their potential as biomarkers, with limited success. There is value in protein biomarkers as complementary to polynucleotide biomarkers. Reasons for having the information provided by both types of biomarkers include the current observations that mRNA expression levels are not good predictors of protein expression levels, and that mRNA expression levels tell nothing of the post-translational modifications of proteins that are key to their biological activity. Therefore, in order to understand the expression levels of proteins, and their complete structure, the direct analysis of proteins is required.

FIGS 2A-2B show an exemplary panel of biomarkers from the list of 22 biomarkers for which gene expression levels are compared in the mouse MIN model, and in human subjects. The selection for the panel is taken from across the list of the 22 biomarkers and is taken for the purpose of easy visual assimilation of data in order to demonstrate the utility of a panel. Typically, for complex data sets represented in the 22 member panel of biomarkers, multivariate analysis (MANOVA) is applied, such as that demonstrated in **FIG 2c**.

In **FIG 2A**, the data reported for the mouse MIN studies represent statistical averaging of a number of animal subjects, and the standard error is reported. The p value on the right indicates the degree of confidence that the values are significantly different. As an example, the first gene listed, SDF-1, is related to the human IL-8 gene, and is in the same super family. For SDF-1, the p value of 0.003 indicates that the probability that the differences in the values of the wildtype control and that of the adenomous polyps of the MIN mice occurred by chance alone is only 3 in 1000. Screening the expression levels in adenomous polyps in the subject mice was specifically targeted, since it has been established that adenomous polyps are useful in risk assessment for CRC. What is demonstrated in **FIG**

2A is that the panel of 6 clearly differentiate the results of the MIN mice over that of the wildtype control.

FIGS 2B-2C address the issue of selectivity for biomarker panels.

Regarding biomarkers that have an acceptable level of selectivity for CRC, the incidence of CRC for individuals in families with a history of CRC is 3-4 times that of the general population. However, It is now estimated that 6% of all Americans will develop CRC, and of those 70-80% will occur in people of average risk. There is clearly a need for biomarkers that have the necessary selectivity required for confidence in the determination of CRC.

In **FIG 2B**, the same panel of 6 biomarkers established in the mouse MIN model in **FIG 2A** are the basis for determination of CRC in human subjects. In **FIG 2B**, the results of biopsy tissue determined to be normal by histological evaluation taken from patients known to have CRC are compared to biopsy tissue from individuals validated as normal controls. It should be noted that histological methodologies are the accepted standard for the identification of a cancerous colonic lesion. There are two aspects of **FIG 2B** to further discuss. First, values for gene expression profiling for patient vs. normal control may vary either up, as in the case of IL 8, or down, as in the case of PPAR- δ . It is the determination of the collective shift for the patient vs. normal control that is significant when using a panel of biomarkers. Second, in glancing through the patient data, sample-to-sample variation can be noted, which is anticipated, given all the patient-to-patient variables. It is clear at a glance that the expression levels for the panel taken as a group distinguish the patient samples overall from the normal control group, even though a value for any one specific biomarker may not in itself distinguish the patient sample from the normal control. For example, the patient designated as H008 has an expression level for PPAR- δ that is not distinct from the normal control. However, at a glance it is clear that the results of the panel for H008 distinguish it from the normal control set. This demonstrates in principle why a validated panel of markers, given the

complexity and variability of biology, enhance the selectivity of a determination vs. a single marker alone.

Fig 2c further serves to emphasize the value of a panel of biomarkers in enhancing the selectivity of a determination between patient vs. normal samples. An example of demonstrating the use of MANOVA for a panel of 9 biomarkers selected from the group of 22 is demonstrated in **Fig 2c**. In this study, 78 sigmoidal-rectal biopsies from 12 normal patients, and 63 sigmoidal-rectal biopsies from non-cancerous sections of 6 patients with sigmoidal-rectal carcinoma were compared. The Wilks' Lambda criterion was used to assess the difference between the patient samples and normal control samples using the 9 biomarkers listed. The lambda value close to 1.0 signifies a significant difference between the patient and normal samples is indicated, with the probability of about 9 chances in 1000 that the difference is by chance alone.

FIGS 3A-3C and **FIGS 4A-4C** address the issue of sensitivity for biomarker panels. As previously mentioned, since survival rates are greatly enhanced with the earliest indication of CRC, biomarkers for risk assessment and early detection of CRC have been long sought. The difference between risk assessment and early detection is the degree of certainty regarding acquiring CRC. Biomarkers that are used for risk assessment confer less than 100% certainty of CRC within a time interval, whereas biomarkers used for early detection confer an almost 100% certainty of the onset of the disease within a specified time interval. Risk factors may be used as surrogate end points for individuals not diagnosed with cancer, providing they there is an established relationship between the surrogate end point and a definitive outcome. An example of an established surrogate end point for CRC is the example of adenomous polyps. What has been established is that the occurrence of adenomous polyps are a necessary, but not sufficient condition for an individual to later develop CRC. This is demonstrated by the fact that 90% percent of all preinvasive

cancerous lesions are adenomous polyps or precursors, but not all individuals with adenomous polyps go on to later develop CRC.

FIGS 3A-3C show graphs of gene expression levels taken for multiple biopsy samples taken from the colon of one exemplary patient diagnosed with CRC. The determination of cancerous lesions, polyps, and adjacent tissues was made by conventional histological methods. The expression levels for three of the panel of biomarkers are shown for the biopsy samples categorized in that fashion. Again, as was demonstrated with the examples given in **FIGS 2A-2C**, it is evident that the three markers taken together for the cancerous lesions sampled are significantly different than the normal controls, even though one by itself (CXCR2) would not have been differentiating for this patient. What is additionally indicated in this representation is the distinction between the results of the polyp vs. the normal control. Given that polyps are already accepted as surrogate endpoints for CRC, then a determination of the presence of polyps by a validated analytical methodology using a minimally invasive method, such as a swab, or a non-invasive sampling method, such as a stool sample, would also serve as surrogate end point for risk assessment.

FIGS 4A-4C show the results of gene expression levels for three of the biomarkers in biopsy samples taken over a 53 cm region of the colon of a patient with CRC. The irregularly shaped objects represent biopsy samples that were confirmed to be cancerous lesions by histological methodology, while the oval shapes represent samples that were determined to be non-cancerous by histological methodology. Gene expression profiling was done for each of the biopsy samples, as well. The results of the expression profiling, where the legend indicates relative levels in the patient biopsy samples as compared to normal controls, are depicted in **FIGS 4A-4C**.

The representation of **FIGS 4A-4C** indicates the distance over which the biomarkers are able to distinguish differences in the colon tissue for the patient, where these biopsy samples were rendered normal by conventional

histological analysis. These results demonstrate that it is possible to sample cells through a minimally invasive swabbing collection method from an area distant from a cancerous lesion, but capable of indicating a non-normal colon condition. Moreover, collection of a stool sample is an already validated sampling method for collecting sloughed cells or cell debris from which these determinations may be made. In that regard, samples taken either minimally invasively or non-invasively would render samples that could be analyzed using the disclosed panel of biomarkers. Such non-invasive procedures not only reduce the cost of determination of CRC, but reduce the discomfort and risk associated with current methodology. All these factors together increase the attractiveness of regular testing, and hence patient compliance. Increased patient compliance, coupled with an effective determination for CRC, enhance the prospects for early detection, and enhanced survival rates.

Methods and kits for the polynucleotide and polypeptide expression profiling for the panel of molecular markers are also contemplated as part of the present disclosure.

In one embodiment, a method for gene expression profiling comprises measuring cDNA levels for biomarkers selected in the claimed panel. Such a method requires the use of primers, enzymes, and other reagents for the preparation, detection, and quantitation of cDNAs. The method of creating cDNA from mRNA in a sample is referred to as the reverse transcriptase polymer chain reaction (RT-PCR). The primers listed in SEQ ID NOs 45-88 are particularly suited for use in gene expression profiling using RT-PCR based on the claimed panel. A series of primers were designed using Primer Express Software (Applied Biosystems, Foster City, CA). Specific candidates were chosen, and then tested to verify that only cDNA was amplified, and not contaminated by genomic DNA. The primers listed in SEQ ID NOs 45-88 were specifically designed, selected, and tested accordingly. In addition to the primers, reagents such as one including a dinucleotide triphosphate

mixture having all four dinucleotide triphosphates (e.g. dATP, dGTP, dCTP, and dTTP), one having the reverse transcriptase enzyme, and one having a thermostable DNA polymerase are required for RT-PCR. Additionally buffers, inhibitors and activators are also required for the RT-PCR process.

5 Once the cDNA has been sufficiently amplified to a specified end point, the cDNA sample must be prepared for detection and quantitation. Though a number of detection schemes are contemplated, as will be discussed in more detail below, one method contemplated for detection of polynucleotides is fluorescence spectroscopy, and therefore chromophores
10 that are suited to fluorescence spectroscopy are desirable for labeling polynucleotides. One example of such a fluorescent label is SYBR Green, though numerous related chromophores exist, and are known in the art.

In another embodiment, a method for protein expression profiling comprises using an antibody panel based on the claimed panel of
15 biomarkers for measuring targeted polypeptide levels from a biological sample. In one embodiment contemplated for the method, the antibodies for the panel are bound to a solid support. The method for protein expression profiling may use a second antibody having specificity to some portion of the bound polypeptide. Such a second antibody may be labeled with molecules
20 useful for detection and quantitation of the bound polypeptides, and therefore in binding to the polypeptide label it for detection and quantitation. Additionally, other reagents are contemplated for labeling the bound polypeptides for detection and quantitation. Such reagents may either directly label the bound polypeptide or, analogous to a second antibody, may
25 be a moiety with specificity for the bound polypeptide having labels. Examples of such moieties include but are not limited to small molecules such as cofactors, substrates, complexing agents, and the like, or large molecules, such as lectins, peptides, oligonucleotides, and the like. Such moieties may be either naturally occurring or synthetic.

30 Examples of detection modes contemplated for the disclosed

5 methods include, but are not limited to spectroscopic techniques, such as fluorescence and UV-Vis spectroscopy, scintillation counting, and mass spectroscopy. Complementary to these modes of detection, examples of labels for the purpose of detection and quantitation used in these methods include, but are not limited to chromophoric labels, scintillation labels, and mass labels. The expression levels of polynucleotides and polypeptides measured using these methods may be normalized to a control established for the purpose of the targeted determination. These methods are believed useful in providing determinations as the basis of effective management of patient care for CRC. These methods may also be used in the discovery of therapeutic interventions for CRC. Additionally, not only biopsy samples from sigmoidoscopy, colonoscopy, or surgery may be analyzed by these methods, but biological samples from non-invasive or minimally evasive collection methods are indicated for these methods, as well.

15 It is further contemplated in what is disclosed to provide kits having the reagents and procedures that facilitate the ready implementation of the methods, and provide consistency and quality control thereby.

In one embodiment, a kit for gene expression profiling comprises the reagents and instructions necessary for the gene expression profiling of the claimed panel. Thus, for example, the reagents may include primers, enzymes, and other reagents for the preparation, detection, and quantitation of cDNAs for the claimed panel of biomarkers. As discussed above, the method of creating cDNA from mRNA in a sample is referred to as the reverse transcriptase polymer chain reaction (RT-PCR). The primers listed in SEQ ID NOs 45-88 are particularly suited for use in gene expression profiling using RT-PCR based on the claimed panel. The primers listed in SEQ ID NOs 45-88 were specifically designed, selected, and tested accordingly. In addition to the primers, reagents such as one including a dinucleotide triphosphate mixture having all four dinucleotide triphosphates (e.g. dATP, dGTP, dCTP, and dTTP), one having the reverse transcriptase

enzyme, and one having a thermostable DNA polymerase are required for RT-PCR. Additionally buffers, inhibitors and activators used for the RT-PCR process are suitable reagents for inclusion in the kit embodiment. Once the cDNA has been sufficiently amplified to a specified end point, the cDNA sample must be prepared for detection and quantitation. One method contemplated for detection of polynucleotides is fluorescence spectroscopy, and therefore chromophores that are suited to fluorescence spectroscopy are desirable for labeling polynucleotides and may also be included in reagents of the kit embodiment. Instructions included with the kit embodiment for gene expression profiling preferably teach the user the following steps: to obtain a biological sample; to isolate cellular RNA from the sample; to amplify copies of cDNA from the sample for each biomarker in the panel, and the panel for which the reagents are provided; and to quantify levels of cDNA amplified from the sample. Though tissue samples from a variety of procedures may be used, the instructions for obtaining a biological sample are preferably whereby the user obtains a sample of colorectal cells in a minimally invasive manner, such as by use of a swab or collection of a stool sample. The instructions may also preferably include the step of comparing the cDNA levels quantified to a control.

In another embodiment, a kit for protein expression profiling comprises the reagents and instructions necessary for protein expression profiling of the claimed panel. Thus, in this embodiment, the kit for protein expression profiling includes supplying an antibody panel based on the claimed panel of biomarkers for measuring targeted polypeptide levels from a biological sample. One embodiment contemplated for such a panel includes the antibody panel bound to a solid support. Additionally, the reagents included with the kit for protein expression profiling may use a second antibody having specificity to some portion of the bound polypeptide. Such a second antibody may be labeled with molecules useful for detection and quantitation of the bound polypeptides, and therefore in binding to the

polypeptide label it for detection and quantitation. Additionally, other reagents are contemplated for labeling the bound polypeptides for detection and quantitation. Such reagents may either directly label the bound polypeptide or, analogous to a second antibody, may be a moiety with specificity for the bound polypeptide having labels. Examples of such moieties include but are not limited to small molecules such as cofactors, substrates, complexing agents, and the like, or large molecules, such as lectins, peptides, oligonucleotides, and the like. Such moieties may be either naturally occurring or synthetic. Instructions for the protein expression profiling kit preferably teach the user: to obtain a biological sample; to use the antibody panel supplied with the kit for each biomarker in the panel to bind the polypeptides from the sample; and to quantify levels of polypeptides bound from the sample to the antibody panel. Preferably, the kit instructions also include a step of comparing the polypeptide levels to a control. Preferably the biological sample is obtained by a minimally invasive procedure such as use of a swab to through a stool sample.

Additionally, consumable labware required for sample collection, preparation, and analysis may be provided with the kits.

What has been disclosed herein has been provided for the purposes of illustration and description. It is not intended to be exhaustive or to limit what is disclosed to the precise forms described. Many modifications and variations will be apparent to the practitioner skilled in the art. What is disclosed was chosen and described in order to best explain the principles and practical application of the disclosed embodiments of the art described, thereby enabling others skilled in the art to understand the various embodiments and various modifications that are suited to the particular use contemplated. It is intended that the scope of what is disclosed be defined by the following claims and their equivalence.

What Is Claimed:

1. A panel of biomarkers for colorectal cancer and colorectal polyps comprising at least two polynucleotides selected from SEQ ID NOs 1-5.
2. The panel of claim 1, where the panel is selected for analysis of polynucleotide expression levels for colorectal cancer and colorectal polyps.
3. The panel of claim 2, where the polynucleotide expression levels are mRNAs.
4. The panel of claim 2, where the polynucleotide expression levels are cDNAs.
5. The panel of claim 1, where at least one of the polynucleotides is a fragment.
6. The panel of claim 1, where at least one of the polynucleotides is a variant.
7. The panel of claim 1, where the panel is used for the management of patient care in colorectal cancer and colorectal polyps.
8. The panel of claim 7, where the management of patient care includes one or more of risk assessment, early diagnosis, establishing prognosis, monitoring patient treatment, and detecting relapse.
9. The panel of claim 1, where the panel is used in discovery of therapeutic intervention of colorectal cancer and colorectal polyps.

10. A panel of biomarkers for colorectal cancer and colorectal polyps comprising:
 - at least two polynucleotides selected from SEQ ID NOs 1-5; and
 - at least one polynucleotide selected from SEQ ID NOs 6-14
11. The panel of claim 10, where the panel is selected for analysis of polynucleotide expression levels for colorectal cancer and colorectal polyps.
12. The panel of claim 11, where the polynucleotide expression levels are mRNAs.
13. The panel of claim 11, where the polynucleotide expression levels are cDNAs.
14. The panel of claim 10, where at least one of the polynucleotides is a fragment.
15. The panel of claim 10, where at least one of the polynucleotides is a variant.
16. The panel of claim 10, where the panel is used in the management of patient care for colorectal cancer and colorectal polyps.
17. The panel of claim 16, where the management of patient care includes one or more of risk assessment, early diagnosis, establishing prognosis, monitoring patient treatment, and detecting relapse.
18. The panel of claim 10, where the panel is used in discovery of therapeutic intervention of colorectal cancer and colorectal polyps.

19. A panel of biomarkers for colorectal cancer and colorectal polyps comprising:
- at least two polynucleotides selected from SEQ ID NOs 1-5;
 - at least one polynucleotide selected from SEQ ID NOs 6-14; and
 - at least one polynucleotide selected from SEQ ID NOs 15-22.
20. The panel of claim 19, where the panel is selected for analysis of polynucleotide expression levels for colorectal cancer and colorectal polyps.
21. The panel of claim 20, where the polynucleotide expression levels are mRNAs.
22. The panel of claim 20, where the polynucleotide expression levels are cDNAs.
23. The panel of claim 19, where at least one of the polynucleotides is a fragment.
24. The panel of claim 19, where at least one of the polynucleotides is a variant.
25. The panel of claim 25, where the panel is the basis for management of patient care in colorectal cancer and colorectal polyps.
26. The panel of claim 19, where the management of patient care includes one or more of risk assessment, early diagnosis, establishing prognosis, monitoring patient treatment, and detecting relapse.

27. The panel of claim 25, where the panel is used in discovery of therapeutic intervention of colorectal cancer and colorectal polyps.
28. A panel of biomarkers for colorectal cancer and colorectal polyps comprising at least two polypeptides selected from SEQ ID NOs 23-27.
29. The panel of claim 28, where the panel is selected for analysis of polypeptide expression levels for colorectal cancer and colorectal polyps.
30. The panel of claim 28, where at least one of the polypeptides is a fragment.
31. The panel of claim 28, where at least one of the polypeptides is a variant.
32. The panel of claim 28, where the panel is used in the management of patient care in colorectal cancer and colorectal polyps.
33. The panel of claim 32, where the management of patient care includes one or more of risk assessment, early diagnosis, establishing prognosis, monitoring patient treatment, and detecting relapse.
34. The panel of claim 28, where the panel is used in discovery of therapeutic intervention of colorectal cancer and colorectal polyps.
35. A panel of biomarkers for colorectal cancer and colorectal polyps comprising:
at least two polypeptides selected from SEQ ID NOs 23-27; and
at least one polypeptide selected from SEQ ID NOs 28-36.

36. The panel of claim 35, where the panel is selected for analysis of polypeptide expression levels for colorectal cancer and colorectal polyps.
37. The panel of claim 35, where at least one of the polypeptides is a fragment.
38. The panel of claim 35, where at least one of the polypeptides is a variant.
39. The panel of claim 35, where the panel is used in the management of patient care in colorectal cancer and colorectal polyps.
40. The panel of claim 39, where the management of patient care includes one or more of risk assessment, early diagnosis, establishing prognosis, monitoring patient treatment, and detecting relapse.
41. The panel of claim 35, where the panel is used in discovery of therapeutic intervention of colorectal cancer and colorectal polyps.
42. A panel of biomarkers for colorectal cancer and colorectal polyps comprising:
at least two polypeptides selected from SEQ ID NOs 23-27;
at least one polypeptide selected from SEQ ID NOs 28-36; and
at least one polypeptide selected from SEQ ID NOs 37-44.
43. The panel of claim 42, where the panel is selected for analysis of polypeptide expression levels for colorectal cancer and colorectal polyps.

44. The panel of claim 42, where at least one of the polypeptides is a fragment.
45. The panel of claim 42, where at least one of the polypeptides is a variant.
46. The panel of claim 42, where the panel is used in the management of patient care in colorectal cancer and colorectal polyps.
47. The panel of claim 46, where the management of patient care includes one or more of risk assessment, early diagnosis, establishing prognosis, monitoring patient treatment, and detecting relapse.
48. The panel of claim 42, where the panel is used in discovery of therapeutic intervention of colorectal cancer and colorectal polyps.
49. A method for measuring expression levels of polynucleotides from biomarkers for colorectal cancer and colorectal polyps, comprising:
selecting a panel of biomarkers comprising at least two polynucleotides from SEQ ID NOs 1-5;
obtaining a biological sample;
isolating cellular RNA from the sample;
amplifying copies of cDNA from the sample for each biomarker in the panel; and
quantifying levels of cDNA amplified from the sample.
50. The method of claim 49, where the step of selecting a panel of biomarkers further comprises at least one polynucleotide from SEQ ID NOs 6-14.

51. The method of claim 49, where the step of selecting a panel of biomarkers further comprises:
- at least one polynucleotide from SEQ ID NOs 6-14; and
 - at least one polynucleotide from SEQ ID NOs 15-22.
52. The method of claim 49, where the step of amplifying copies of cDNA further comprises at least two sets of primers chosen from SEQ. ID NOs 45-50.
53. The method of claim 52, where the step of amplifying copies of cDNA further comprises using enzymes and reagents for the preparation of cDNAs.
54. The method of claim 49, where the step of quantifying the levels of cDNA further comprises labeling cDNA.
55. The method of claim 54, where labeling cDNA includes at least one chromophore.
56. The method of claim 49, where the cDNA levels for the sample are compared to a control.
57. The method of claim 56, where the comparison is used in the management of patient care in colorectal cancer and colorectal polyps.
58. The method of claim 57, where the management of patient care includes one or more of risk assessment, early diagnosis, establishing prognosis, monitoring patient treatment, and detecting relapse.

59. The method of claim 56, where the comparison is used in discovery of therapeutic intervention of colorectal cancer and colorectal polyps.

60. The method of claim 49, where the step of obtaining a biological sample is by obtaining a sample of colorectal cells.

61. The method of claim 60, where the step of obtaining a sample of colorectal cells is minimally invasive.

62. The method of claim 61, where the minimally invasive step is by use of a swab.

63. The method of claim 60, where the step of obtaining a sample of colorectal cells is non-invasive.

64. The method of claim 63, where the non-invasive step is by collection of a stool sample.

65. A method for measuring expression levels of polypeptides from biomarkers for colorectal cancer and colorectal cancer, comprising:
selecting a panel of biomarkers comprising at least two polypeptides from SEQ ID NOs 23-27;
obtaining a biological sample;
creating an antibody panel for each biomarker in the panel;
using the antibody panel to bind the polypeptides from the sample;
and
quantifying levels of polypeptides bound from the sample to the antibody panel.

66. The method of claim 65, where the step of selecting a panel of biomarkers further comprises at least one polypeptide from SEQ ID NOs 28-36.

67. The method of claim 65, where the step of selecting a panel of biomarkers further comprises:

at least one polypeptide from SEQ ID NOs 28-36; and

at least one polypeptide from SEQ ID NOs 37-44.

68. The method of claim 65, where the polypeptide levels for the sample are compared to a control.

69. The method of claim 68, where the comparison is used in the management of patient care in colorectal cancer and colorectal polyps.

70. The method of claim 69, where the management of patient care includes one or more of risk assessment, early diagnosis, establishing prognosis, monitoring patient treatment, and detecting relapse.

71. The method of claim 68, where the comparison is used in discovery of therapeutic intervention of colorectal cancer and colorectal polyps.

72. The method of claim 65, where the step of obtaining a biological sample is by obtaining a sample of colorectal cells.

73. The method of claim 72, where the step of obtaining a sample of colorectal cells is minimally invasive.

74. The method of claim 73, where the minimally invasive step is by use of a swab.

75. The method of claim 72, where the step of obtaining a sample of colorectal cells is non-invasive.

76. The method of claim 75, where the non-invasive step is by collection of a stool sample.

77. The method of claim 65, where the step of quantifying the bound polypeptides further comprises labeling the polypeptides.

78. The method of claim 77, where labeling the polypeptides comprises using a second antibody.

79. A kit for the determination of colorectal cancer and colorectal polyps comprising:

at least one reagent that is used in analysis of polynucleotide expression levels for a panel of biomarkers for colorectal cancer and colorectal polyps, where the panel comprises at least two polynucleotides listed in SEQ ID NOs 1-5; and

instructions for using the kit for analyzing the expression levels.

80. The kit of claim 79, where the panel of biomarkers further comprises at least one polynucleotides listed in SEQ ID NOs 6-14.

81. The kit of claim 79, where the panel of biomarkers further comprises:
at least one polynucleotide selected from SEQ ID NOs 6-14; and
at least one polynucleotide selected from SEQ ID NOs 15-22.

82. The kit of claim 79, where the polynucleotide expression levels are mRNAs.
83. The kit of claim 79, where the polynucleotide expression levels are cDNAs.
84. The kit of claim 83, where the reagent comprises at least two sets of primers chosen from SEQ. ID NOs 45-50.
85. The kit of claim 84, further comprising reagents for the preparation of cDNA.
86. The kit of claim 79, comprising a reagent that is used for detection and quantitation of polynucleotides.
87. The kit of claim 86, where the reagent includes at least one chromophore.
88. The kit of claim 79, further comprising consumable labware for at least one of sample collection, sample preparation, and sample analysis.
89. A kit for the determination of colorectal cancer and colorectal polyps comprising:
at least one reagent used in that analysis of polypeptide expression levels for a panel of biomarkers for colorectal cancer and colorectal polyps, where the panel comprises at least two polypeptides listed in SEQ. ID NOs 23-27; and
instructions for using the kit for analyzing the expression levels.

90. The kit of claim 89, where the panel of biomarkers further comprises at least one polynucleotides listed in SEQ ID NOs 28-36.
91. The kit of claim 89, where the panel of biomarkers further comprises:
at least one polynucleotide selected from SEQ ID NOs 28-36; and
at least one polynucleotide selected from SEQ ID NOs 37-44.
92. The kit of claim 89, where the reagent is an antibody reagent that binds a polypeptide selected in the panel.
93. The kit of claim 89, further comprising a reagent that is used for detection and quantitation of a bound polypeptide.
94. The kit of claim 93, where the reagent includes a second antibody.
95. The kit of claim 89, further comprising consumable labware for at least one of sample collection, sample preparation, and sample analysis.

Sequence ID No. / ID	NCBI Entrez Database	Name	Abbreviation
1. Coding sequence	XM_031289	Interleukin 8	IL8
2. Coding sequence	XM_051900	Prostaglandin-endoperoxide synthase 2	PTGS2
3. Coding sequence	M94582	Interleukin 8 receptor B	ILR8RB
4. Coding sequence	NM_005555	Lipocalin 2	LCN2
5. Coding sequence	NM_000331	Serum amyloid A1	SAA1
6. Coding sequence	NM_000757	Macrophage colony stimulating factor 1	CSF1 (MCSF1)
7. Coding sequence	X54489	Melanoma growth stimulatory activity	MGSA
8. Coding sequence	NM_002090	Chemokine (C-X-C motif) ligand 3	CXCL3
9. Coding sequence	XM_032429	Secreted phosphoprotein 1	SPP1 (OPN)
10. Coding sequence	M64349	Cyclin D	CCND1
11. Coding sequence	AX057136	c-Myc	c-Myc
12. Coding sequence	L25610	Cyclin-dependent kinase inhibitor	HUMCDK1
13. Coding sequence	BC021998	Cyclin-dependent kinase inhibitor 2A	CDKN2A
14. Coding sequence	NM_058195	Alternative reading frame p14	CDKN2A
15. Coding sequence	NM_005036	Peroxisome proliferative activated receptor, alpha	PPARA
16. Coding sequence	XM_003059	Peroxisome proliferative activated receptor, gamma	PPARG
17. Coding sequence	NM_006238	Peroxisome proliferative activated receptor, delta	PPARD
18. Coding sequence	XM_030326	CD44 antigen	CD44
19. Coding sequence	XM_044882	Prostaglandin-endoperoxide synthase 1	PTGS1
20. Coding sequence	NM_002131	High-mobility group AT-hook1 isoform B	HMGAI
21. Coding sequence	X54942	CKSHS2	CKSHS2
22. Coding sequence	U22055	100 kDa coactivator	p100 coactivator
23. Protein	XP_031289	Interleukin 8	IL8
24. Protein	XP_051900	Prostaglandin-endoperoxide synthase 2	COX2
25. Protein	AA36108	Interleukin 8 receptor B	CXCR2
26. Protein	NP_005555	Lipocalin 2	LCN2
27. Protein	NP_000331	Serum amyloid A1	SAA1
28. Protein	NP_000757	Macrophage colony stimulating factor 1	MCSF1
29. Protein	CAA38361	Melanoma growth stimulatory activity	Groα
30. Protein	NM-002090	Chemokine (C-X-C motif) ligand 3	Groγ

Figure 1

Sequence ID No. / ID	NCBI Entrez Database	Name	Abbreviation
31. Protein	XP_032429	Osteopontin	OPN
32. Protein	AAA52136	Cyclin D	cyclin D1
33. Protein	CAC22425	c-Myc	c-Myc
34. Protein	AAA16109	Cyclin-dependent kinase inhibitor	p21
35. Protein	AAH21998	Cyclin-dependent kinase inhibitor 2A	p16
36. Protein	NP_047862	Alternative reading frame p14	p14ARF
37. Protein	NP_005027	Peroxisome proliferative activated receptor, alpha	PPAR α
38. Protein	XP_003059	Peroxisome proliferative activated receptor, gamma	PPAR γ
39. Protein	NP_006229	Peroxisome proliferative activated receptor, delta	PPAR δ
40. Protein	XP_030326	CD44 antigen	CD44
41. Protein	XP_044882	Prostaglandin-endoperoxide synthase 1	COX1
42. Protein	NP_002122	High-mobility group AT-hook1 isoform B	HYGY1
43. Protein	CAA38703	CKS1 protein homolog	CKS1
44. Protein	AAA80488	100 kDa coactivator	p100 coactivator
45. Forward primer		Interleukin 8	IL8
46. Reverse primer			
47. Forward primer		Prostaglandin-endoperoxide synthase 2	PTGS2
48. Reverse primer			
49. Forward primer		Interleukin 8 receptor B	ILR8RB
50. Reverse primer			
51. Forward primer		Lipocalin 2	LCN2
52. Reverse primer			
53. Forward primer		Serum amyloid A1	SAA1
54. Reverse primer			
55. Forward primer		Macrophage colony stimulating factor 1	CSF1 (MCSF1)
56. Reverse primer			
57. Forward primer		Melanoma growth stimulatory activity	MGSA
58. Reverse primer			
59. Forward primer		Chemokine (C-X-C motif) ligand 3	MGSA
60. Reverse primer			

Figure 1 – cont'd

Sequence ID No. / ID	NCBI Entrez Database	Name	Abbreviation
61. Forward primer		Secreted phosphoprotein 1	SPP1 (OPN)
62. Reverse primer			
63. Forward primer		Cyclin D	CCND1
64. Reverse primer			
65. Forward primer		c-Myc	c-Myc
66. Reverse primer			
67. Forward primer		Cyclin-dependent kinase inhibitor	HUMCDK1
68. Reverse primer			
69. Forward primer		Cyclin-dependent kinase inhibitor 2A	CDKN2A
70. Reverse primer			
71. Forward primer		Alternative reading frame p14	CDKN2A
72. Reverse primer			
73. Forward primer		Peroxisome proliferative activated receptor, alpha	PPAR α
74. Reverse primer			
75. Forward primer		Peroxisome proliferative activated receptor, gamma	PPAR γ
76. Reverse primer			
77. Forward primer		Peroxisome proliferative activated receptor, delta	PPAR δ
78. Reverse primer			
79. Forward primer		CD44 antigen	CD44
80. Reverse primer			
81. Forward primer		Prostaglandin-endoperoxide synthase 1	COX1
82. Reverse primer			
83. Forward primer		High-mobility group AT-hook1 isoform B	HMGY1
84. Reverse primer			
85. Forward primer		CKS1 protein homolog	CKS1
86. Reverse primer			
87. Forward primer		100 kDa coactivator	p100 coactivator
88. Reverse primer			

Figure 1 – cont'd

4/6

Relative Gene Expression Levels in Colon Polyps (Average \pm SE)

No.	Genes	Wild-Type Littermate	Individual Poly	P Value
1	SDF-1	1.23 \pm 0.34	11.02 \pm 2.45	0.003
2	COX2	1.41 \pm 0.25	87.48 \pm 16.50	<0.001
3	CXCR2	1.41 \pm 0.35	11221 \pm 23.76	<0.001
4	OPN	1.62 \pm 0.60	463.37 \pm 130.49	0.004
5	MCSFI	1.05 \pm 0.15	4.26 \pm 1.60	0.08
6	PPAR δ	1.16 \pm 0.27	0.44 \pm 0.05	0.04

FIG. 2A

Relative Gene Expressions in Normal-Appearing Mucosa from Colon Cancer

	Sigmoid and Rectum						Ascending Colon			
	NB	H002	H004	H006	H008	H011	NB	H003	H009	H010
IL-8	1.80 \pm 0.26	28.91	7.14	6.88	18.35	24.67	1.72 \pm 0.35	16.03	4.90	28.26
COX2	1.85 \pm 0.29	13.54	10.34	18.23	14.63	1.87	1.74 \pm 0.45	25.48	11.98	33.06
CXCR2	1.31 \pm 0.14	11.35	6.82	6.85	7.18	100.20	1.26 \pm 0.17	10.23	22.62	11.20
OPN	2.11 \pm 0.52	10.85	9.84	11.88	21.29	3.41	1.43 \pm 0.20	26.83	23.97	64.13
MCSF1	1.69 \pm 0.19	4.49	11.88	12.84	7.24	7.98	1.57 \pm 0.22	12.40	17.89	14.97
PPAR- δ	1.14 \pm 0.07	0.10	0.09	0.12	1.28	0.96	1.16 \pm 0.11	0.09	1.10	0.30

FIG. 2B

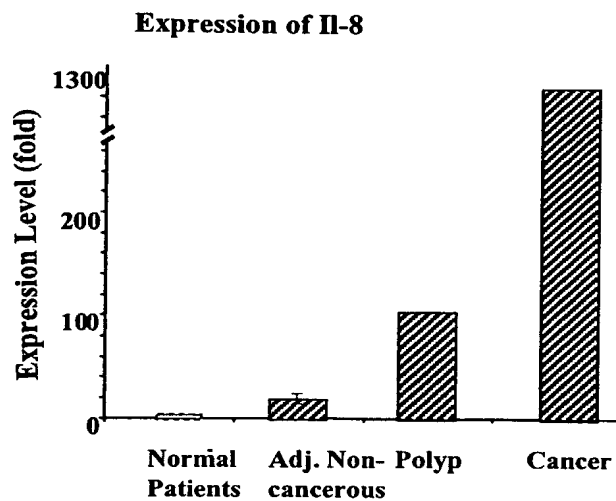
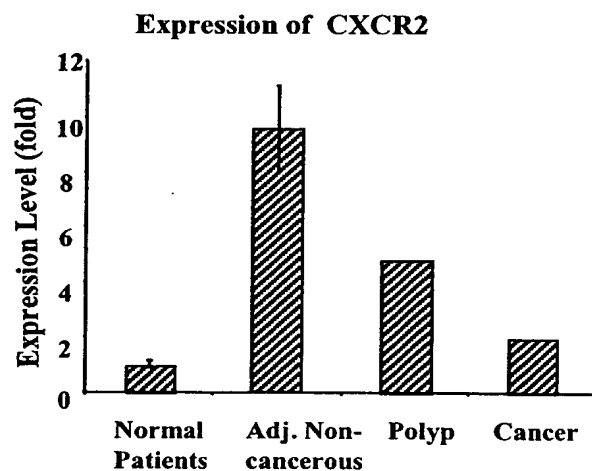
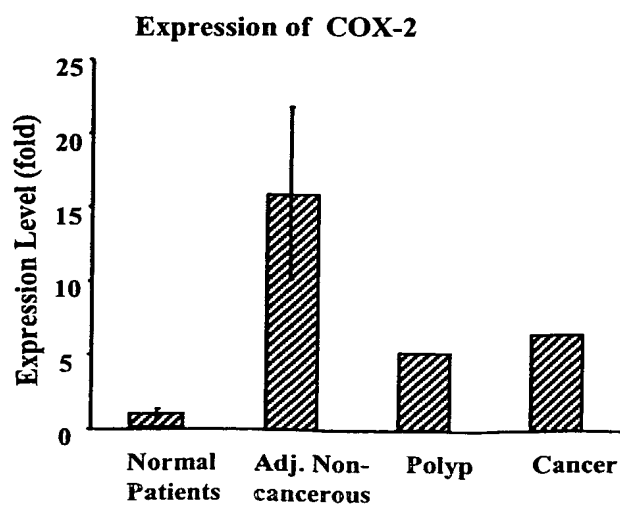
Dependent Variable: IL-8, M-CSF-1, COX-2, OPN, p21, PPAR- γ , CXCR2, CD44, PPAR- δ

Results for Multivariate Analysis: Wilks Lambda Criterion

Source	Lambda	probability
Cancer	0.989	0.0086

FIG. 2C

5/6

**Fig. 3A****Fig. 3B****Fig. 3C**

6/6

IL-8

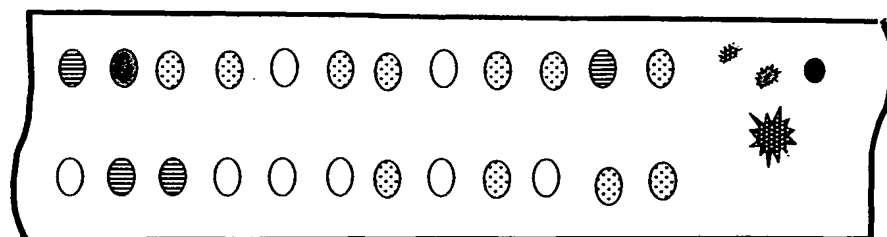


Fig. 4A



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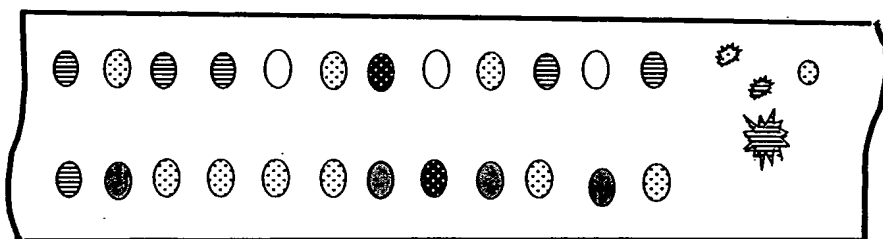


Fig. 4B



53 cm

CXCR2

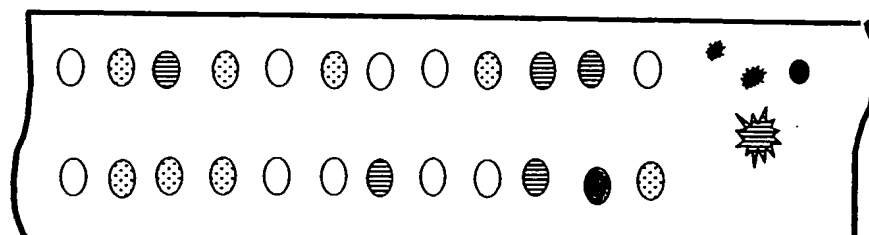


Fig. 4C



53 cm

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2/88

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3/88

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			185				190				195						
gat	cat	aag	cga	ggg	cca	gct	ttc	acc	aac	ggg	ctg	ggc	cat	ggg	gtg	739	
Asp	His	Lys	Arg	Gly	Pro	Ala	Phe	Thr	Asn	Gly	Leu	Gly	His	Gly	Val		
			200				205				210						
gac	tta	aat	cat	att	tac	ggg	gaa	act	ctg	gct	aga	cag	cgt	aaa	ctg	787	
Asp	Leu	Asn	His	Ile	Tyr	Gly	Glu	Thr	Leu	Ala	Arg	Gln	Arg	Lys	Leu		
			215				220				225				230		

4/88

cgc ctt ttc aag gat gga aaa atg aaa tat cag ata att gat gga gag	835
Arg Leu Phe Lys Asp Gly Lys Met Lys Tyr Gln Ile Ile Asp Gly Glu	
235 240 245	
atg tat cct ccc aca gtc aaa gat act cag gca gag atg atc tac cct	883
Met Tyr Pro Pro Thr Val Lys Asp Thr Gln Ala Glu Met Ile Tyr Pro	
250 255 260	
cct caa gtc cct gag cat cta cgg ttt gct gtg ggg cag gag gtc ttt	931
Pro Gln Val Pro Glu His Leu Arg Phe Ala Val Gly Gln Glu Val Phe	
265 270 275	
ggg ctg gtg cct ggt ctg atg atg tat gcc aca atc tgg ctg cgg gaa	979
Gly Leu Val Pro Gly Leu Met Met Tyr Ala Thr Ile Trp Leu Arg Glu	
280 285 290	
cac aac aga gta tgc gat gtg ctt aaa cag gag cat cct gaa tgg ggt	1027
His Asn Arg Val Cys Asp Val Leu Lys Gln Glu His Pro Glu Trp Gly	
295 300 305 310	
gat gag cag ttg ttc cag aca agc agg cta ata ctg ata gga gag act	1075
Asp Glu Gln Leu Phe Gln Thr Ser Arg Leu Ile Leu Ile Gly Glu Thr	
315 320 325	
att aag att gtg att gaa gat tat gtg caa cac ttg agt ggc tat cac	1123
Ile Lys Ile Val Ile Glu Asp Tyr Val Gln His Leu Ser Gly Tyr His	
330 335 340	
ttc aaa ctg aaa ttt gac cca gaa cta ctt ttc aac aaa caa ttc cag	1171
Phe Lys Leu Lys Phe Asp Pro Glu Leu Leu Phe Asn Lys Gln Phe Gln	
345 350 355	
tac caa aat cgt att gct gct gaa ttt aac acc ctc tat cac tgg cat	1219
Tyr Gln Asn Arg Ile Ala Ala Glu Phe Asn Thr Leu Tyr His Trp His	
360 365 370	
ccc ctt ctg cct gac acc ttt caa att cat gac cag aaa tac aac tat	1267
Pro Leu Leu Pro Asp Thr Phe Gln Ile His Asp Gln Lys Tyr Asn Tyr	
375 380 385 390	
caa cag ttt atc tac aac aac tct ata ttg ctg gaa cat gga att acc	1315
Gln Gln Phe Ile Tyr Asn Asn Ser Ile Leu Leu Glu His Gly Ile Thr	
395 400 405	
cag ttt gtt gaa tca ttc acc agg caa att gct ggc agg gtt gct ggt	1363
Gln Phe Val Glu Ser Phe Thr Arg Gln Ile Ala Gly Arg Val Ala Gly	
410 415 420	
ggg agg aat gtt cca ccc gca gta cag aaa gta tca cag gct tcc att	1411
Gly Arg Asn Val Pro Pro Ala Val Gln Lys Val Ser Gln Ala Ser Ile	
425 430 435	
gac cag agc agg cag atg aaa tac cag tct ttt aat gag tac cgc aaa	1459
Asp Gln Ser Arg Gln Met Lys Tyr Gln Ser Phe Asn Glu Tyr Arg Lys	
440 445 450	

5/88

cgc ttt atg ctg aag ccc tat gaa tca ttt gaa gaa ctt aca gga gaa 1507
 Arg Phe Met Leu Lys Pro Tyr Glu Ser Phe Glu Glu Leu Thr Gly Glu
 455 460 465 470

aag gaa atg tct gca gag ttg gaa gca ctc tat ggt gac atc gat gct 1555
 Lys Glu Met Ser Ala Glu Leu Glu Ala Leu Tyr Gly Asp Ile Asp Ala
 475 480 485

gtg gag ctg tat cct gcc ctt ctg gta gaa aag cct cgg cca gat gcc 1603
 Val Glu Leu Tyr Pro Ala Leu Leu Val Glu Lys Pro Arg Pro Asp Ala
 490 495 500

atc ttt ggt gaa acc atg gta gaa gtt gga gca cca ttc tcc ttg aaa 1651
 Ile Phe Gly Glu Thr Met Val Glu Val Gly Ala Pro Phe Ser Leu Lys
 505 510 515

gga ctt atg ggt aat gtt ata tgt tct cct gcc tac tgg aag cca agc 1699
 Gly Leu Met Gly Asn Val Ile Cys Ser Pro Ala Tyr Trp Lys Pro Ser
 520 525 530

act ttt ggt gga gaa gtg ggt ttt caa atc atc aac act gcc tca att 1747
 Thr Phe Gly Gly Glu Val Gly Phe Gln Ile Ile Asn Thr Ala Ser Ile
 535 540 545 550

cag tct ctc atc tgc aat aac gtg aag ggc tgt ccc ttt act tca ttc 1795
 Gln Ser Leu Ile Cys Asn Asn Val Lys Gly Cys Pro Phe Thr Ser Phe
 555 560 565

agt gtt cca gat cca gag ctc att aaa aca gtc acc atc aat gca agt 1843
 Ser Val Pro Asp Pro Glu Leu Ile Lys Thr Val Thr Ile Asn Ala Ser
 570 575 580

tct tcc cgc tcc gga cta gat gat atc aat ccc aca gta cta cta aaa 1891
 Ser Ser Arg Ser Gly Leu Asp Asp Ile Asn Pro Thr Val Leu Leu Lys
 585 590 595

gaa cgt tcg act gaa ctg tagaagtcta atgatcatat ttatttatatt 1939
 Glu Arg Ser Thr Glu Leu
 600

atatgaacca tgtctattaa tttaattatt taataatatt tatattaaac tccttatgtt 1999
 acttaacatc ttctgtaaca gaagtcagta ctctgttgc ggagaaagga gtcatacttg 2059
 tgaagacttt tatgtcacta ctctaaagat ttgtgtgttg ctgttaagtt tggaaaacag 2119
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 caacttatat tataagaacg aaagtaaaga tgtttgaata cttaaact gtcacaagat 2239
 ggcaaaatgc tgaaagtttt tacactgtcg atgtttccaa tgcacttcc atgatgcatt 2299
 agaagtaact aatgtttgaa attttaaagt acttttggtt atttttctgt catcaaaca 2359
 aaacaggtat cagtgcatta ttaaataaat atttaaatta gacattacca gtaatttcat 2419
 gtctactttt taaaatcagc aatgaaacaa taatttgaaa tttctaaatt catagggtag 2479

6/88

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aatcacctgt aaaagcttgt ttgatttctt aaagttatta aacttgtaga tataacaaaa 2539
agaagctgtc ttggatttaa atctgtaaaa tcagtagaaa ttttactaca attgcttggt 2599
aaaatatttt ataagtgatg ttcccttttc accaagagta taaacctttt tagtgtgact 2659
gttaaaactt cctttttaa caaaatgcc aatttattaa ggtggtggag ccaactgcagt 2719
gttatcttaa aataagaata ttttggtgag atattccaga atttggttat atggctggta 2779
acatgtaaaa tctatatcag caaaagggc tacctttaa ataagcaata acaaagaaga 2839
aaaccaaatt attgttcaa tttaggttta aacttttgaa gcaaactttt ttttatcctt 2899
gtgcactgca ggctggtac tcagattttg ctatgaggtt aatgaagtac caagctgtgc 2959
ttgaataatg atatgttttc tcagattttc tgttgtagag ttttaatttag cagtccatat 3019
cacattgcaa aagtagcaat gacctcataa aatacctctt caaaatgctt aaattcattt 3079
cacacattaa ttttatctca gtcttgaagc caattcagta ggtgcattgg aatcaagcct 3139
ggctacctgc atgctgttcc ttttcttttc ttcttttagc cattttgcta agagacacag 3199
tcttctcatc acttcgtttc tcctattttg ttttactagt ttaagatca gagttcactt 3259
tctttggact ctgcctatat tttcttacct gaacttttgc aagttttcag gtaaacctca 3319
gctcaggact gctatttagc tcctcttaag aagatta 3356

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<210> 3
 <211> 1750
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (53)..(1132)

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<400> 3
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                                         Met Glu
                                         1

gat ttt aac atg gag agt gac agc ttt gaa gat ttc tgg aaa ggt gaa 106
Asp Phe Asn Met Glu Ser Asp Ser Phe Glu Asp Phe Trp Lys Gly Glu
      5                      10                      15

gat ctt agt aat tac agt tac agc tct acc ctg ccc cct ttt cta cta 154
Asp Leu Ser Asn Tyr Ser Tyr Ser Ser Thr Leu Pro Pro Phe Leu Leu
      20                      25                      30

gat gcc gcc cca tgt gaa cca gaa tcc ctg gaa atc aac aag tat ttt 202
Asp Ala Ala Pro Cys Glu Pro Glu Ser Leu Glu Ile Asn Lys Tyr Phe
      35                      40                      45                      50

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7/88

gtg gtc att atc tat gcc ctg gta ttc ctg ctg agc ctg ctg gga aac	250
Val Val Ile Ile Tyr Ala Leu Val Phe Leu Leu Ser Leu Leu Gly Asn	
55 60 65	
tcc ctc gtg atg ctg gtc atc tta tac agc agg gtc ggc cgc tcc gtc	298
Ser Leu Val Met Leu Val Ile Leu Tyr Ser Arg Val Gly Arg Ser Val	
70 75 80	
act gat gtc tac ctg ctg aac cta gcc ttg gcc gac cta ctc ttt gcc	346
Thr Asp Val Tyr Leu Leu Asn Leu Ala Leu Ala Asp Leu Leu Phe Ala	
85 90 95	
ctg acc ttg ccc atc tgg gcc gcc tcc aag gtg aat ggc tgg att ttt	394
Leu Thr Leu Pro Ile Trp Ala Ala Ser Lys Val Asn Gly Trp Ile Phe	
100 105 110	
ggc aca ttc ctg tgc aag gtg gtc tca ctc ctg aag gaa gtc aac ttc	442
Gly Thr Phe Leu Cys Lys Val Val Ser Leu Leu Lys Glu Val Asn Phe	
115 120 125 130	
tat agt ggc atc ctg cta ctg gcc tgc atc agt gtg gac cgt tac ctg	490
Tyr Ser Gly Ile Leu Leu Leu Ala Cys Ile Ser Val Asp Arg Tyr Leu	
135 140 145	
gcc att gtc cat gcc aca cgc aca ctg acc cag aag cgc tac ttg gtc	538
Ala Ile Val His Ala Thr Arg Thr Leu Thr Gln Lys Arg Tyr Leu Val	
150 155 160	
aaa ttc ata tgt ctc agc atc tgg ggt ctg tcc ttg ctc ctg gcc ctg	586
Lys Phe Ile Cys Leu Ser Ile Trp Gly Leu Ser Leu Leu Leu Ala Leu	
165 170 175	
cct gtc tta ctt ttc cga agg acc gtc tac tca tcc aat gtt agc cca	634
Pro Val Leu Leu Phe Arg Arg Thr Val Tyr Ser Ser Asn Val Ser Pro	
180 185 190	
gcc tgc tat gag gac atg ggc aac aat aca gca aac tgg cgg atg ctg	682
Ala Cys Tyr Glu Asp Met Gly Asn Asn Thr Ala Asn Trp Arg Met Leu	
195 200 205 210	
tta cgg atc ctg ccc cag tcc ttt ggc ttc atc gtg cca ctg ctg atc	730
Leu Arg Ile Leu Pro Gln Ser Phe Gly Phe Ile Val Pro Leu Leu Ile	
215 220 225	
atg ctg ttc tgc tac gga ttc acc ctg cgt acg ctg ttt aag gcc cac	778
Met Leu Phe Cys Tyr Gly Phe Thr Leu Arg Thr Leu Phe Lys Ala His	
230 235 240	
atg ggg cag aag cac cgg gcc atg cgg gtc atc ttt gct gtc gtc ctc	826
Met Gly Gln Lys His Arg Ala Met Arg Val Ile Phe Ala Val Val Leu	
245 250 255	
atc ttc ctg ctt tgc tgg ctg ccc tac aac ctg gtc ctg ctg gca gac	874
Ile Phe Leu Leu Cys Trp Leu Pro Tyr Asn Leu Val Leu Leu Ala Asp	
260 265 270	

8/88

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acc ctc atg agg acc cag gtg atc cag gag acc tgt gag cgc cgc aat 922
Thr Leu Met Arg Thr Gln Val Ile Gln Glu Thr Cys Glu Arg Arg Asn
275                280                285                290

cac atc gac cgg gct ctg gat gcc acc gag att ctg ggc atc ctt cac 970
His Ile Asp Arg Ala Leu Asp Ala Thr Glu Ile Leu Gly Ile Leu His
                295                300                305

agc tgc ctc aac ccc ctc atc tac gcc ttc att ggc cag aag ttt cgc 1018
Ser Cys Leu Asn Pro Leu Ile Tyr Ala Phe Ile Gly Gln Lys Phe Arg
                310                315                320

cat gga ctc ctc aag att cta gct ata cat ggc ttg atc agc aag gac 1066
His Gly Leu Leu Lys Ile Leu Ala Ile His Gly Leu Ile Ser Lys Asp
                325                330                335

tcc ctg ccc aaa gac agc agg cct tcc ttt gtt ggc tct tct tca ggg 1114
Ser Leu Pro Lys Asp Ser Arg Pro Ser Phe Val Gly Ser Ser Ser Gly
                340                345                350

cac act tcc act act ctc taagacctcc tgccctaagtg cagccccgtg 1162
His Thr Ser Thr Thr Leu
355                360

gggttctctc cttctcttca cagtcacatt ccaagcctca tgtccactgg ttcttcttgg 1222

tctcagtgtc aatgcagccc ccattgtggt cacaggaagc agaggaggcc acgttcttac 1282

tagtttccct tgcattggtt agaaagcttg ccttggtgcc tcaccccttg ccataattac 1342

tatgtcattt gctggagctc tgcccatcct gcccctgagc ccatggcact ctatgttcta 1402

agaagtgaaa atctacactc cagtgaagaca gctctgcata ctcattagga tggctagtat 1462

caaaagaaag aaaatcaggc tggccaacgg gatgaaaccc tgtctctact aaaaatacaa 1522

aaaaaaaaaa aaaaattagc cgggcgtggt ggtgagtgcc tgtaatcaca gctacttggg 1582

aggctgagat ggagagaatca cttgaacccg ggaggcagag gttgcagtga gccgagattg 1642

tgcccctgca ctccagcctg agcgacagtg agactctgtc tcagtccatg aagatgtaga 1702

ggagaaactg gaactctcga gcgttgctgg gggggattgt aaaatggt 1750

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<211> 597
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(597)

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Met Pro Leu Gly Leu Leu Trp Leu Gly Leu Ala Leu Leu Gly Ala Leu
1                5                10                15

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9/88

cat gcc cag gcc cag gac tcc acc tca gac ctg atc cca gcc cca cct	96
His Ala Gln Ala Gln Asp Ser Thr Ser Asp Leu Ile Pro Ala Pro Pro	
20 25 30	
ctg agc aag gtc cct ctg cag cag aac ttc cag gac aac caa ttc cag	144
Leu Ser Lys Val Pro Leu Gln Gln Asn Phe Gln Asp Asn Gln Phe Gln	
35 40 45	
ggg aag tgg tat gtg gta ggc ctg gca ggg aat gca att ctc aga gaa	192
Gly Lys Trp Tyr Val Val Gly Leu Ala Gly Asn Ala Ile Leu Arg Glu	
50 55 60	
gac aaa gac ccg caa aag atg tat gcc acc atc tat gag ctg aaa gaa	240
Asp Lys Asp Pro Gln Lys Met Tyr Ala Thr Ile Tyr Glu Leu Lys Glu	
65 70 75 80	
gac aag agc tac aat gtc acc tcc gtc ctg ttt agg aaa aag aag tgt	288
Asp Lys Ser Tyr Asn Val Thr Ser Val Leu Phe Arg Lys Lys Lys Cys	
85 90 95	
gac tac tgg atc agg act ttt gtt cca ggt tgc cag ccc ggc gag ttc	336
Asp Tyr Trp Ile Arg Thr Phe Val Pro Gly Cys Gln Pro Gly Glu Phe	
100 105 110	
acg ctg ggc aac att aag agt tac cct gga tta acg agt tac ctc gtc	384
Thr Leu Gly Asn Ile Lys Ser Tyr Pro Gly Leu Thr Ser Tyr Leu Val	
115 120 125	
cga gtg gtg agc acc aac tac aac cag cat gct atg gtg ttc ttc aag	432
Arg Val Val Ser Thr Asn Tyr Asn Gln His Ala Met Val Phe Phe Lys	
130 135 140	
aaa gtt tct caa aac agg gag tac ttc aag atc acc ctc tac ggg aga	480
Lys Val Ser Gln Asn Arg Glu Tyr Phe Lys Ile Thr Leu Tyr Gly Arg	
145 150 155 160	
acc aag gag ctg act tcg gaa cta aag gag aac ttc atc cgc ttc tcc	528
Thr Lys Glu Leu Thr Ser Glu Leu Lys Glu Asn Phe Ile Arg Phe Ser	
165 170 175	
aaa tat ctg ggc ctc cct gaa aac cac atc gtc ttc cct gtc cca atc	576
Lys Tyr Leu Gly Leu Pro Glu Asn His Ile Val Phe Pro Val Pro Ile	
180 185 190	
gac cag tgt atc gac ggc tga	597
Asp Gln Cys Ile Asp Gly	
195	

<210> 5

<211> 369

<212> DNA

<213> Homo sapiens

10/88

<220>

<221> CDS

<222> (1)..(369)

<400> 5

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atg aag ctt ctc acg ggc ctg gtt ttc tgc tcc ttg gtc ctg ggt gtc 48
Met Lys Leu Leu Thr Gly Leu Val Phe Cys Ser Leu Val Leu Gly Val
  1             5             10             15

agc agc cga agc ttc ttt tcg ttc ctt ggc gag gct ttt gat ggg gct 96
Ser Ser Arg Ser Phe Phe Ser Phe Leu Gly Glu Ala Phe Asp Gly Ala
          20             25             30

cgg gac atg tgg aga gcc tac tct gac atg aga gaa gcc aat tac atc 144
Arg Asp Met Trp Arg Ala Tyr Ser Asp Met Arg Glu Ala Asn Tyr Ile
          35             40             45

ggc tca gac aaa tac ttc cat gct cgg ggg aac tat gat gct gcc aaa 192
Gly Ser Asp Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Lys
          50             55             60

agg gga cct ggg ggt gtc tgg gct gca gaa gcg atc agc gat gcc aga 240
Arg Gly Pro Gly Gly Val Trp Ala Ala Glu Ala Ile Ser Asp Ala Arg
          65             70             75             80

gag aat atc cag aga ttc ttt ggc cat ggt gcg gag gac tcg ctg gct 288
Glu Asn Ile Gln Arg Phe Phe Gly His Gly Ala Glu Asp Ser Leu Ala
          85             90             95

gat cag gct gcc aat gaa tgg ggc agg agt ggc aaa gac ccc aat cac 336
Asp Gln Ala Ala Asn Glu Trp Gly Arg Ser Gly Lys Asp Pro Asn His
          100             105             110

ttc cga cct gct ggc ctg cct gag aaa tac tga 369
Phe Arg Pro Ala Gly Leu Pro Glu Lys Tyr
          115             120

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<210> 6

<211> 3939

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (106)..(1767)

<400> 6

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gccgggggcgc ccaactccgca gcagccagcg agccagctgc cccgt atg acc gcg ccg 117
Met Thr Ala Pro
          1

ggc gcc gcc ggg cgc tgc cct ccc acg aca tgg ctg ggc tcc ctg ctg 165
Gly Ala Ala Gly Arg Cys Pro Pro Thr Thr Trp Leu Gly Ser Leu Leu
  5             10             15             20

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ttg	ttg	gtc	tgt	ctc	ctg	gcg	agc	agg	agt	atc	acc	gag	gag	gtg	tcg	213
Leu	Leu	Val	Cys	Leu 25	Leu	Ala	Ser	Arg	Ser 30	Ile	Thr	Glu	Glu	Val 35	Ser	
gag	tac	tgt	agc	cac	atg	att	ggg	agt	gga	cac	ctg	cag	tct	ctg	cag	261
Glu	Tyr	Cys	Ser 40	His	Met	Ile	Gly	Ser 45	Gly	His	Leu	Gln	Ser 50	Leu	Gln	
cgg	ctg	att	gac	agt	cag	atg	gag	acc	tcg	tgc	caa	att	aca	ttt	gag	309
Arg	Leu	Ile 55	Asp	Ser	Gln	Met	Glu 60	Thr	Ser	Cys	Gln	Ile 65	Thr	Phe	Glu	
ttt	gta	gac	cag	gaa	cag	ttg	aaa	gat	cca	gtg	tgc	tac	ctt	aag	aag	357
Phe	Val 70	Asp	Gln	Glu	Gln	Leu 75	Lys	Asp	Pro	Val	Cys 80	Tyr	Leu	Lys	Lys	
gca	ttt	ctc	ctg	gta	caa	gac	ata	atg	gag	gac	acc	atg	cgc	ttc	aga	405
Ala 85	Phe	Leu	Leu	Val 90	Gln	Asp	Ile	Met	Glu	Asp 95	Thr	Met	Arg	Phe	Arg 100	
gat	aac	acc	gcc	aat	ccc	atc	gcc	att	gtg	cag	ctg	cag	gaa	ctc	tct	453
Asp	Asn	Thr	Ala 105	Asn	Pro	Ile	Ala	Ile	Val 110	Gln	Leu	Gln	Glu	Leu 115	Ser	
ttg	agg	ctg	aag	agc	tgc	ttc	acc	aag	gat	tat	gaa	gag	cat	gac	aag	501
Leu	Arg	Leu	Lys 120	Ser	Cys	Phe	Thr	Lys 125	Asp	Tyr	Glu	Glu	His 130	Asp	Lys	
gcc	tgc	gtc	cga	act	ttc	tat	gag	aca	cct	ctc	cag	ttg	ctg	gag	aag	549
Ala	Cys	Val 135	Arg	Thr	Phe	Tyr	Glu 140	Thr	Pro	Leu	Gln	Leu 145	Leu	Glu	Lys	
gtc	aag	aat	gtc	ttt	aat	gaa	aca	aag	aat	ctc	ctt	gac	aag	gac	tggt	597
Val	Lys 150	Asn	Val	Phe	Asn	Glu 155	Thr	Lys	Asn	Leu	Leu 160	Asp	Lys	Asp	Trp	
aat	att	ttc	agc	aag	aac	tgc	aac	aac	agc	ttt	gct	gaa	tgc	tcc	agc	645
Asn 165	Ile	Phe	Ser	Lys	Asn 170	Cys	Asn	Asn	Ser	Phe 175	Ala	Glu	Cys	Ser	Ser 180	
caa	gat	gtg	gtg	acc	aag	cct	gat	tgc	aac	tgc	ctg	tac	ccc	aaa	gcc	693
Gln	Asp	Val	Val 185	Thr	Lys	Pro	Asp	Cys	Asn 190	Cys	Leu	Tyr	Pro	Lys 195	Ala	
atc	cct	agc	agt	gac	ccg	gcc	tct	gtc	tcc	cct	cat	cag	ccc	ctc	gcc	741
Ile	Pro	Ser 200	Ser	Asp	Pro	Ala	Ser	Val 205	Ser	Pro	His	Gln	Pro 210	Leu	Ala	
ccc	tcc	atg	gcc	cct	gtg	gct	ggc	ttg	acc	tggt	gag	gac	tct	gag	gga	789
Pro	Ser	Met 215	Ala	Pro	Val	Ala	Gly 220	Leu	Thr	Trp	Glu	Asp 225	Ser	Glu	Gly	
act	gag	ggc	agc	tcc	ctc	ttg	cct	ggt	gag	cag	ccc	ctg	cac	aca	gtg	837
Thr 230	Glu	Gly	Ser	Ser	Leu 235	Leu	Pro	Gly	Glu	Gln 240	Pro	Leu	His	Thr	Val	

12/88

gat cca ggc agt gcc aag cag cgg cca ccc agg agc acc tgc cag agc	885
Asp Pro Gly Ser Ala Lys Gln Arg Pro Pro Arg Ser Thr Cys Gln Ser	
245 250 255 260	
ttt gag ccg cca gag acc cca gtt gtc aag gac agc acc atc ggt ggc	933
Phe Glu Pro Pro Glu Thr Pro Val Val Lys Asp Ser Thr Ile Gly Gly	
265 270 275	
tca cca cag cct cgc ccc tct gtc ggg gcc ttc aac ccc ggg atg gag	981
Ser Pro Gln Pro Arg Pro Ser Val Gly Ala Phe Asn Pro Gly Met Glu	
280 285 290	
gat att ctt gac tct gca atg ggc act aat tgg gtc cca gaa gaa gcc	1029
Asp Ile Leu Asp Ser Ala Met Thr Asn Trp Val Pro Glu Glu Ala	
295 300 305	
tct gga gag gcc agt gag att ccc gta ccc caa ggg aca gag ctt tcc	1077
Ser Gly Glu Ala Ser Glu Ile Pro Val Pro Gln Gly Thr Glu Leu Ser	
310 315 320	
ccc tcc agg cca gga ggg ggc agc atg cag aca gag ccc gcc aga ccc	1125
Pro Ser Arg Pro Gly Gly Gly Ser Met Gln Thr Glu Pro Ala Arg Pro	
325 330 335 340	
agc aac ttc ctc tca gca tct tct cca ctc cct gca tca gca aag ggc	1173
Ser Asn Phe Leu Ser Ala Ser Ser Pro Leu Pro Ala Ser Ala Lys Gly	
345 350 355	
caa cag ccg gca gat gta act gct aca gcc ttg ccc agg gtg ggc ccc	1221
Gln Gln Pro Ala Asp Val Thr Ala Thr Ala Leu Pro Arg Val Gly Pro	
360 365 370	
gtg atg ccc act ggc cag gac tgg aat cac acc ccc cag aag aca gac	1269
Val Met Pro Thr Gly Gln Asp Trp Asn His Thr Pro Gln Lys Thr Asp	
375 380 385	
cat cca tct gcc ctg ctc aga gac ccc ccg gag cca ggc tct ccc agg	1317
His Pro Ser Ala Leu Leu Arg Asp Pro Pro Glu Pro Gly Ser Pro Arg	
390 395 400	
atc tca tca ctg cgc ccc cag gcc ctc agc aac ccc tcc acc ctc tct	1365
Ile Ser Ser Leu Arg Pro Gln Ala Leu Ser Asn Pro Ser Thr Leu Ser	
405 410 415 420	
gct cag cca cag ctt tcc aga agc cac tcc tcg ggc agc gtg ctg ccc	1413
Ala Gln Pro Gln Leu Ser Arg Ser His Ser Ser Gly Ser Val Leu Pro	
425 430 435	
ctt ggg gag ctg gag ggc agg agg agc acc agg gat cgg acg agc ccc	1461
Leu Gly Glu Leu Glu Gly Arg Arg Ser Thr Arg Asp Arg Thr Ser Pro	
440 445 450	
gca gag cca gaa gca gca cca gca agt gaa ggg gca gcc agg ccc ctg	1509
Ala Glu Pro Glu Ala Ala Pro Ala Ser Glu Gly Ala Ala Arg Pro Leu	
455 460 465	

13/88

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ccc cgt ttt aac tcc gtt cct ttg act gac aca ggc cat gag agg cag 1557
Pro Arg Phe Asn Ser Val Pro Leu Thr Asp Thr Gly His Glu Arg Gln
    470                475                480

tcc gag gga tcc tcc agc ccg cag ctc cag gag tct gtc ttc cac ctg 1605
Ser Glu Gly Ser Ser Ser Pro Gln Leu Gln Glu Ser Val Phe His Leu
485                490                495                500

ctg gtg ccc agt gtc atc ctg gtc ttg ctg gct gtc gga ggc ctc ttg 1653
Leu Val Pro Ser Val Ile Leu Val Leu Leu Ala Val Gly Gly Leu Leu
                    505                510                515

ttc tac agg tgg agg cgg cgg agc cat caa gag cct cag aga gcg gat 1701
Phe Tyr Arg Trp Arg Arg Arg Ser His Gln Glu Pro Gln Arg Ala Asp
                    520                525                530

tct ccc ttg gag caa cca gag ggc agc ccc ctg act cag gat gac aga 1749
Ser Pro Leu Glu Gln Pro Glu Gly Ser Pro Leu Thr Gln Asp Asp Arg
    535                540                545

cag gtg gaa ctg cca gtg tagaggggaat tctaagctgg acgcacagaa 1797
Gln Val Glu Leu Pro Val
    550

cagtctcttc gtgggaggag acattatggg gcgtccacca ccacctctcc ctggccatcc 1857

tcctggaatg tgggtctgcc tccaccagag ctctgcctg ccaggactgg accagagcag 1917

ccaggctggg gccctctgt ctcaaccgc agaccctga ctgaatgaga gaggccagag 1977

gatgctcccc atgctgccac tatctattgt gagccctgga ggctcccatg tgcttgagga 2037

aggctggtga gcccggtca ggacctctt cctcagggg ctgcagcctc ctctactcc 2097

cttccatgcc ggaaccagg ccagggaccc accggcctgt ggtttgtggg aaagcagggg 2157

gcacgctgag gagtgaaca accctgcacc cagagggcct gcctggtgcc aaggtatccc 2217

agcctggaca ggcattggacc tgtctccaga cagaggagcc tgaagtctgt ggggcgggac 2277

agcctcggcc tgatttccc taaagggtgt cagcctgaga gacgggaaga ggaggcctct 2337

gcacctgctg gtctgcactg acagcctgaa gggctctacac cctcggctca cctaagtccc 2397

tgtgctgggt gccaggccca gaggggaggg cagccctgcc ctccaggacct gcctgacctg 2457

ccagtgatgc caagaggggg atcaagcact ggctctgcc cctcctcctt ccagcacctg 2517

ccagagcttc tccagcaggc caagcagagg ctccctcat gaaggaagcc attgcactgt 2577

gaacactgta cctgcctgct gaacagcctc ccccgctcca tccatgagcc agcatccgtc 2637

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tgagggagcc cctcagccct gaccttctcc tgacctggcc tttgactccc cggagtggag 2757

tgggggtggga gaacctcctg ggccgccagc cagagccgct ctttaggctg tgttcttcgc 2817

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14/88

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ccagggtttct gcatcttcca ctttgacatt cccaagagggg aagggactag tgggagagag 2877
caagggagggg gagggcacag acagagagcc tacagggcga gctctgactg aagatggggc 2937
tttgaaatat aggtatgcac ctgaggttgg gggaggggtct gcactcccaa accccagcgc 2997
agtgtccttt ccctgctgcc gacaggaacc tggggctgag cagggttatcc ctgtcaggag 3057
ccctggactg ggctgcatct cagccccacc tgcattggtat ccagctccca tccactttctc 3117
acccttcttt cctcctgacc ttggtcagca gtgatgacct ccaactctca cccaccccct 3177
ctaccatcac ctctaaccag gcaagccagg gtgggagagc aatcaggaga gccaggcctc 3237
agcttccaat gcctggaggg cctccacttt gtggccagcc tgtgggtgctg gctctgaggc 3297
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gccacctctg gtgtcccca ggctacctgc tcaggaaccc cttctgttct ctgagaactc 3777
aacagaggac attggctcac gcaactgtgag attttgtttt tatacttgca actggtgaat 3837
tattttttat aaagtcattt aaatatctat taaaagata ggaagctgct tatatatatta 3897
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```

<210> 7

<211> 1024

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(321)

<400> 7

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atg gcc cgc gct gct ctc tcc gcc gcc ccc agc aat ccc cgg ctc ctg 48
Met Ala Arg Ala Ala Leu Ser Ala Ala Pro Ser Asn Pro Arg Leu Leu
  1             5             10             15

cga gtg gca ctg ctg ctc ctg ctc ctg gta gcc gct ggc cgg cgc gca 96
Arg Val Ala Leu Leu Leu Leu Leu Val Ala Ala Gly Arg Arg Ala
      20             25             30

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15/88

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gca gga gcg tcc gtg gcc act gaa ctg cgc tgc cag tgc ttg cag acc 144
Ala Gly Ala Ser Val Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr
      35              40              45

ctg cag gga att cac ccc aag aac atc caa agt gtg aac gtg aag tcc 192
Leu Gln Gly Ile His Pro Lys Asn Ile Gln Ser Val Asn Val Lys Ser
      50              55              60

ccc gga ccc cac tgc gcc caa acc gaa gtc ata gcc aca ctc aag aat 240
Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn
      65              70              75              80

ggg cgg aaa gct tgc ctc aat cct gca tcc ccc ata gtt aag aaa atc 288
Gly Arg Lys Ala Cys Leu Asn Pro Ala Ser Pro Ile Val Lys Lys Ile
      85              90              95

atc gaa aag atg ctg aac agt gac aaa tcc aac tgaccagaag ggaggaggaa 341
Ile Glu Lys Met Leu Asn Ser Asp Lys Ser Asn
      100              105

gctcactggg ggctgttcct gaaggaggcc ctgcccttat aggaacagaa gaggaaagag 401

agacacagct gcagaggcca cctggattgt gcctaattgtg tttgagcatc gcttaggaga 461

agtcttctat ttatttattt attcattagt tttgaagatt ctatgttaat attttaggtg 521

taaaataaatt aaggggatga ttaactctac ctgcacactg tcctattata ttcattcttt 581

ttgaaatgtc aacccaagt tagttcaatc tggattcata tttaatttga aggtagaatg 641

ttttcaaatg ttctccagtc attatgttaa tatttctgag gagcctgcaa catgccagcc 701

actgtgatag aggctggcgg atccaagcaa atggccaatg agatcattgt gaaggcaggg 761

gaatgtatgt gcacatctgt tttgtaactg tttagatgaa tgtcagttgt tatttattga 821

aatgatttca cagtgtgtgg tcaacatttc tcatgttgaa actttaagaa ctaaaatggt 881

ctaaatatcc cttggacatt ttatgtcttt cttgtaagga atactgcctt gtttaatggg 941

agttttacag tgtttctggc ttagaacaaa ggggcttaat tattgatgtt tcatagaga 1001

atataaaaaat aaagcactta tag 1024

```

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<210> 8
<211> 1064
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (78)..(395)

<220>
<221> modified_base

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16/88

<222> (27)

<223> a, c, t, g, other or unknown

<220>

<221> modified_base

<222> (766)

<223> a, c, t, g, other or unknown

<400> 8

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cacagccggg tcgcaggcac ctccccngcc agctctcccg cattctgcac agcttcccga 60

cgcgctctgct gagcccc atg gcc cac gcc acg ctc tcc gcc gcc ccc agc      110
                Met Ala His Ala Thr Leu Ser Ala Ala Pro Ser
                  1             5             10

aat ccc cgg ctc ctg cgg gtg gcg ctg ctg ctc ctg ctc ctg gtg ggc      158
Asn Pro Arg Leu Leu Arg Val Ala Leu Leu Leu Leu Leu Val Gly
                  15             20             25

agc cgg cgc gca gca gga gcg tcc gtg gtc act gaa ctg cgc tgc cag      206
Ser Arg Arg Ala Ala Gly Ala Ser Val Val Thr Glu Leu Arg Cys Gln
                  30             35             40

tgc ttg cag aca ctg cag gga att cac ctc aag aac atc caa agt gtg      254
Cys Leu Gln Thr Leu Gln Gly Ile His Leu Lys Asn Ile Gln Ser Val
                  45             50             55

aat gta agg tcc ccc gga ccc cac tgc gcc caa acc gaa gtc ata gcc      302
Asn Val Arg Ser Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala
                  60             65             70             75

aca ctc aag aat ggg aag aaa gct tgt ctc aac ccc gca tcc ccc atg      350
Thr Leu Lys Asn Gly Lys Lys Ala Cys Leu Asn Pro Ala Ser Pro Met
                  80             85             90

gtt cag aaa atc atc gaa aag ata ctg aac aag ggg agc acc aac      395
Val Gln Lys Ile Ile Glu Lys Ile Leu Asn Lys Gly Ser Thr Asn
                  95             100             105

tgacaggaga gaagtaagaa gcttatcagc gtatcattga cacttcctgc aggggtggtcc 455

ctgcccttac cagagctgaa aatgaaaaag agaacagcag ctttctaggg acagctggaa 515

agggacttaa tgtgtttgac tatttccttac gagggttcta cttatttatg tatttatattt 575

tgaaagcttg tattttaata ttttacatgc tgttatttaa agatgtgagt gtgtttcatc 635

aaacatagct cagtcctgat tatttaattg gaatatgatg ggttttaaat gtgtcattaa 695

actaatatatt agtgggagac cataatgtgt cagccacctt gataaatgac aggggtgggga 755

actggagggt nggggggattg aaatgcaagc aattagtgga tcaactgtag ggtaagggaa 815

tgtatgtaca catctatttt ttatactttt ttttttaaaa aagaatgtca gttgttatatt 875

attcaaatta tctcacatta tgtgttcaac atttttatgc tgaagtttcc cttagacatt 935

ttatgtcttg cttgtagggc ataatgcctt gtttaatgtc cattctgcag cgtttctctt 995

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17/88

tcccttgga aagagaattt atcattactg ttacatttgt acaaatagaca tgataataaa 1055
 agttttatg 1064

<210> 9
 <211> 1469
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (102)..(1001)

<400> 9
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 agccttctca gccaaacgcc gaccaaggaa aactcactac c atg aga att gca gtg 116
 Met Arg Ile Ala Val
 1 5

att tgc ttt tgc ctc cta ggc atc acc tgt gcc ata cca gtt aaa cag 164
 Ile Cys Phe Cys Leu Leu Gly Ile Thr Cys Ala Ile Pro Val Lys Gln
 10 15 20

gct gat tct gga agt tct gag gaa aag cag ctt tac aac aaa tac cca 212
 Ala Asp Ser Gly Ser Ser Glu Glu Lys Gln Leu Tyr Asn Lys Tyr Pro
 25 30 35

gat gct gtg gcc aca tgg cta aac cct gac cca tct cag aag cag aat 260
 Asp Ala Val Ala Thr Trp Leu Asn Pro Asp Pro Ser Gln Lys Gln Asn
 40 45 50

ctc cta gcc cca cag acc ctt cca agt aag tcc aac gaa agc cat gac 308
 Leu Leu Ala Pro Gln Thr Leu Pro Ser Lys Ser Asn Glu Ser His Asp
 55 60 65

cac atg gat gat atg gat gat gaa gat gat gat gac cat gtg gac agc 356
 His Met Asp Asp Met Asp Asp Glu Asp Asp Asp Asp His Val Asp Ser
 70 75 80 85

cag gac tcc att gac tcg aac gac tct gat gat gta gat gac act gat 404
 Gln Asp Ser Ile Asp Ser Asn Asp Ser Asp Asp Val Asp Asp Thr Asp
 90 95 100

gat tct cac cag tct gat gag tct cac cat tct gat gaa tct gat gaa 452
 Asp Ser His Gln Ser Asp Glu Ser His His Ser Asp Glu Ser Asp Glu
 105 110 115

ctg gtc act gat ttt ccc acg gac ctg cca gca acc gaa gtt ttc act 500
 Leu Val Thr Asp Phe Pro Thr Asp Leu Pro Ala Thr Glu Val Phe Thr
 120 125 130

cca gtt gtc ccc aca gta gac aca tat gat ggc cga ggt gat agt gtg 548
 Pro Val Val Pro Thr Val Asp Thr Tyr Asp Gly Arg Gly Asp Ser Val
 135 140 145

18/88

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gtt tat gga ctg agg tca aaa tct aag aag ttt cgc aga cct gac atc 596
Val Tyr Gly Leu Arg Ser Lys Ser Lys Lys Phe Arg Arg Pro Asp Ile
150                      155                      160                      165

cag tac cct gat gct aca gac gag gac atc acc tca cac atg gaa agc 644
Gln Tyr Pro Asp Ala Thr Asp Glu Asp Ile Thr Ser His Met Glu Ser
170                      175                      180

gag gag ttg aat ggt gca tac aag gcc atc ccc gtt gcc cag gac ctg 692
Glu Glu Leu Asn Gly Ala Tyr Lys Ala Ile Pro Val Ala Gln Asp Leu
185                      190                      195

aac gcg cct tct gat tgg gac agc cgt ggg aag gac agt tat gaa acg 740
Asn Ala Pro Ser Asp Trp Asp Ser Arg Gly Lys Asp Ser Tyr Glu Thr
200                      205                      210

agt cag ctg gat gac cag agt gct gaa acc cac agc cac aag cag tcc 788
Ser Gln Leu Asp Asp Gln Ser Ala Glu Thr His Ser His Lys Gln Ser
215                      220                      225

aga tta tat aag cgg aaa gcc aat gat gag agc aat gag cat tcc gat 836
Arg Leu Tyr Lys Arg Lys Ala Asn Asp Glu Ser Asn Glu His Ser Asp
230                      235                      240                      245

gtg att gat agt cag gaa ctt tcc aaa gtc agc cgt gaa ttc cac agc 884
Val Ile Asp Ser Gln Glu Leu Ser Lys Val Ser Arg Glu Phe His Ser
250                      255                      260

cat gaa ttt cac agc cat gaa gat atg ctg gtt gta gac ccc aaa agt 932
His Glu Phe His Ser His Glu Asp Met Leu Val Val Asp Pro Lys Ser
265                      270                      275

aag gaa gaa gat aaa cac ctg aaa ttt cgt att tct cat gaa tta gat 980
Lys Glu Glu Asp Lys His Leu Lys Phe Arg Ile Ser His Glu Leu Asp
280                      285                      290

agt gca tct tct gag gtc aat taaaaggaga aaaaatacaa tttctcactt 1031
Ser Ala Ser Ser Glu Val Asn
295                      300

tgcatttagt caaaagaaaa aatgctttat agcaaatga aagagaacat gaaatgcttc 1091

tttctcagtt tattggttga atgtgtatct atttgagtct ggaaataact aatgtgtttg 1151

ataattagtt tagtttgtgg cttcatggaa actccctgta aactaaaagc ttcagggtta 1211

tgtctatggt cattctatag aagaaatgca aactatcact gtattttaat atttgttatt 1271

ctctcatgaa tagaaattta tgtagaagca aacaaaatac ttttaccac ttaaaaagag 1331

aatataacat tttatgtcac tataatcttt tgttttttaa gttagtgtat atttgttgt 1391

gattatcttt ttgtggtgtg aataaatctt ttatcttgaa tgtaataaga aaaaaaaaaa 1451

aaaaacaaaa aaaaaaaaaa 1469

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<210> 10
<211> 1256
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (145) .. (1029)
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gcgcgggggca	gcagaagcga	gagccgagcg	cggacccagc	caggacccac	agccctcccc	120																
agctgcccag	gaagagcccc	agcc	atg	gaa	cac	cag	ctc	ctg	tgc	tgc	gaa	171										
			Met	Glu	His	Gln	Leu	Leu	Cys	Cys	Glu											
			1				5															
gtg	gaa	acc	atc	cgc	cgc	gcg	tac	ccc	gat	gcc	aac	ctc	ctc	aac	gac	219						
Val	Glu	Thr	Ile	Arg	Arg	Ala	Tyr	Pro	Asp	Ala	Asn	Leu	Leu	Asn	Asp							
10					15					20					25							
cgg	gtg	ctg	cgg	gcc	atg	ctg	aag	gcg	gag	gag	acc	tgc	gcg	ccc	tcg	267						
Arg	Val	Leu	Arg	Ala	Met	Leu	Lys	Ala	Glu	Glu	Thr	Cys	Ala	Pro	Ser							
				30					35					40								
gtg	tcc	tac	ttc	aaa	tgt	gtg	cag	aag	gag	gtc	ctg	ccg	tcc	atg	cgg	315						
Val	Ser	Tyr	Phe	Lys	Cys	Val	Gln	Lys	Glu	Val	Leu	Pro	Ser	Met	Arg							
			45					50					55									
aag	atc	gtc	gcc	acc	tgg	atg	ctg	gag	gtc	tgc	gag	gaa	cag	aag	tgc	363						
Lys	Ile	Val	Ala	Thr	Trp	Met	Leu	Glu	Val	Cys	Glu	Glu	Gln	Lys	Cys							
		60					65					70										
gag	gag	gag	gtc	ttc	ccg	ctg	gcc	atg	aac	tac	ctg	gac	cgc	ttc	ctg	411						
Glu	Glu	Glu	Val	Phe	Pro	Leu	Ala	Met	Asn	Tyr	Leu	Asp	Arg	Phe	Leu							
		75				80					85											
tcg	ctg	gag	ccc	gtg	aaa	aag	agc	cgc	ctg	cag	ctg	ctg	ggg	gcc	act	459						
Ser	Leu	Glu	Pro	Val	Lys	Lys	Ser	Arg	Leu	Gln	Leu	Leu	Gly	Ala	Thr							
	90				95					100					105							
tgc	atg	ttc	gtg	gcc	tct	aag	atg	aag	gag	acc	atc	ccc	ctg	acg	gcc	507						
Cys	Met	Phe	Val	Ala	Ser	Lys	Met	Lys	Glu	Thr	Ile	Pro	Leu	Thr	Ala							
				110					115					120								
gag	aag	ctg	tgc	atc	tac	acc	gac	ggc	tcc	atc	cgg	ccc	gag	gag	ctg	555						
Glu	Lys	Leu	Cys	Ile	Tyr	Thr	Asp	Gly	Ser	Ile	Arg	Pro	Glu	Glu	Leu							
			125					130					135									
ctg	caa	atg	gag	ctg	ctc	ctg	gtg	aac	aag	ctc	aag	tgg	aac	ctg	gcc	603						
Leu	Gln	Met	Glu	Leu	Leu	Leu	Val	Asn	Lys	Leu	Lys	Trp	Asn	Leu	Ala							
		140					145					150										
gca	atg	acc	ccg	cac	gat	ttc	att	gaa	cac	ttc	ctc	tcc	aaa	atg	cca	651						
Ala	Met	Thr	Pro	His	Asp	Phe	Ile	Glu	His	Phe	Leu	Ser	Lys	Met	Pro							
	155					160					165											

20/88

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gag gcg gag gag aac aaa cag atc atc cgc aaa cac gcg cag acc ttc      699
Glu Ala Glu Glu Asn Lys Gln Ile Ile Arg Lys His Ala Gln Thr Phe
170                               175                               180                               185

gtt gcc tct tgt gcc aca gat gtg aag ttc att tcc aat ccg ccc tcc      747
Val Ala Ser Cys Ala Thr Asp Val Lys Phe Ile Ser Asn Pro Pro Ser
                               190                               195                               200

atg gtg gca gcg ggg agc gtg gtg gcc gca gtg caa ggc ctg aac ctg      795
Met Val Ala Ala Gly Ser Val Val Ala Ala Val Gln Gly Leu Asn Leu
                               205                               210                               215

agg agc ccc aac aac ttc ctg tcc tac tac cgc ctc aca cgc ttc ctc      843
Arg Ser Pro Asn Asn Phe Leu Ser Tyr Tyr Arg Leu Thr Arg Phe Leu
                               220                               225                               230

tcc aga gtg atc aag tgt gac cca gac tgc ctc cgg gcc tgc cag gag      891
Ser Arg Val Ile Lys Cys Asp Pro Asp Cys Leu Arg Ala Cys Gln Glu
                               235                               240                               245

cag atc gaa gcc ctg ctg gag tca agc ctg cgc cag gcc cag cag aac      939
Gln Ile Glu Ala Leu Leu Glu Ser Ser Leu Arg Gln Ala Gln Gln Asn
250                               255                               260                               265

atg gac ccc aag gcc gcc gag gag gag gaa gag gag gag gag gag gtg      987
Met Asp Pro Lys Ala Ala Glu Glu Glu Glu Glu Glu Glu Glu Glu Val
                               270                               275                               280

gac ctg gct tgc aca ccc acc gac gtg cgg gac gtg gac atc      1029
Asp Leu Ala Cys Thr Pro Thr Asp Val Arg Asp Val Asp Ile
                               285                               290                               295

tgagggggccc aggcaggcgg gcgccaccgc caccgcgagc gagggcgagg ccggccccag 1089

gtgctccaca tgacagtccc tcctctccgg agcattttga taccagaagg gaaagcttca 1149

ttctccttgt tggtggttgt tttttccttt gctctttccc ccttccatct ctgacttaag 1209

caaaagaaaa agattaccca aaaactgtct ttaaaagaga gagagag      1256

<210> 11
<211> 2121
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (559)..(1875)

<400> 11
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gggcagggct tctcagaggc ttggcgggaa aaaagaacgg agggagggat cgcgctgagt 120

ataaaagccg gttttcgggg ctttatctaa ctgcgtgtag taattccagc gagaggcaga 180

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21/88

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gggagcgagc gggcgcccg ctaggggtgga agagccgggc gagcagagct gcgctgcggg 240
cgtcctggga agggagatcc ggagcgaata gggggcttcg cctctggccc agccctcccg 300
cttgatcccc caggccagcg gtccgcaacc cttgccgcat ccacgaaact ttgcccatag 360
cagcggggcgg gcactttgca ctggaactta caacacccga gcaaggacgc gactctcccg 420
acgcgggggag gctattctgc ccatttgggg acacttcccc gccgctgccca ggaccgcgtt 480
ctctgaaagg ctctccttgc agctgcttag acgctggatt tttttcgggt agtggaanaac 540

cagcagcctc ccgcgacg atg ccc ctc aac gtt agc ttc acc aac agg aac 591
Met Pro Leu Asn Val Ser Phe Thr Asn Arg Asn
1 5 10

tat gac ctc gac tac gac tcg gtg cag ccg tat ttc tac tgc gac gag 639
Tyr Asp Leu Asp Tyr Asp Ser Val Gln Pro Tyr Phe Tyr Cys Asp Glu
15 20 25

gag gag aac ttc tac cag cag cag cag cag agc gag ctg cag ccc ccg 687
Glu Glu Asn Phe Tyr Gln Gln Gln Gln Gln Ser Glu Leu Gln Pro Pro
30 35 40

gcg ccc agc gag gat atc tgg aag aaa ttc gag ctg ctg ccc acc ccg 735
Ala Pro Ser Glu Asp Ile Trp Lys Lys Phe Glu Leu Leu Pro Thr Pro
45 50 55

ccc ctg tcc cct agc cgc cgc tcc ggg ctc tgc tcg ccc tcc tac gtt 783
Pro Leu Ser Pro Ser Arg Arg Ser Gly Leu Cys Ser Pro Ser Tyr Val
60 65 70 75

gcg gtc aca ccc ttc tcc ctt cgg gga gac aac gac ggc ggt ggc ggg 831
Ala Val Thr Pro Phe Ser Leu Arg Gly Asp Asn Asp Gly Gly Gly Gly
80 85 90

agc ttc tcc acg gcc gac cag ctg gag atg gtg acc gag ctg ctg gga 879
Ser Phe Ser Thr Ala Asp Gln Leu Glu Met Val Thr Glu Leu Leu Gly
95 100 105

gga gac atg gtg aac cag agt ttc atc tgc gac ccg gac gac gag acc 927
Gly Asp Met Val Asn Gln Ser Phe Ile Cys Asp Pro Asp Asp Glu Thr
110 115 120

ttc atc aaa aac atc atc atc cag gac tgt atg tgg agc ggc ttc tcg 975
Phe Ile Lys Asn Ile Ile Ile Gln Asp Cys Met Trp Ser Gly Phe Ser
125 130 135

gcc gcc gcc aag ctc gtc tca gag aag ctg gcc tcc tac cag gct gcg 1023
Ala Ala Ala Lys Leu Val Ser Glu Lys Leu Ala Ser Tyr Gln Ala Ala
140 145 150 155

cgc aaa gac agc ggc agc ccg aac ccc gcc cgc ggc cac agc gtc tgc 1071
Arg Lys Asp Ser Gly Ser Pro Asn Pro Ala Arg Gly His Ser Val Cys
160 165 170

```


22/88

tcc acc tcc agc ttg tac ctg cag gat ctg agc gcc gcc gcc tca gag	1119
Ser Thr Ser Ser Leu Tyr Leu Gln Asp Leu Ser Ala Ala Ala Ser Glu	
175 180 185	
tgc atc gac ccc tcg gtg gtc ttc ccc tac cct ctc aac gac agc agc	1167
Cys Ile Asp Pro Ser Val Val Phe Pro Tyr Pro Leu Asn Asp Ser Ser	
190 195 200	
tcg ccc aag tcc tgc gcc tcg caa gac tcc agc gcc ttc tct ccg tcc	1215
Ser Pro Lys Ser Cys Ala Ser Gln Asp Ser Ser Ala Phe Ser Pro Ser	
205 210 215	
tcg gat tct ctg ctc tcc tcg acg gag tcc tcc ccg cag ggc agc ccc	1263
Ser Asp Ser Leu Leu Ser Ser Thr Glu Ser Ser Pro Gln Gly Ser Pro	
220 225 230 235	
gag ccc ctg gtg ctc cat gag gag aca ccg ccc acc acc agc agc gac	1311
Glu Pro Leu Val Leu His Glu Glu Thr Pro Pro Thr Thr Ser Ser Asp	
240 245 250	
tct gag gag gaa caa gaa gat gag gaa gaa atc gat gtt gtt tct gtg	1359
Ser Glu Glu Glu Gln Glu Asp Glu Glu Glu Ile Asp Val Val Ser Val	
255 260 265	
gaa aag agg cag gct cct ggc aaa agg tca gag tct gga tca cct tct	1407
Glu Lys Arg Gln Ala Pro Gly Lys Arg Ser Glu Ser Gly Ser Pro Ser	
270 275 280	
gct gga ggc cac agc aaa cct cct cac agc cca ctg gtc ctc aag agg	1455
Ala Gly Gly His Ser Lys Pro Pro His Ser Pro Leu Val Leu Lys Arg	
285 290 295	
tgc cac gtc tcc aca cat cag cac aac tac gca gcg cct ccc tcc act	1503
Cys His Val Ser Thr His Gln His Asn Tyr Ala Ala Pro Pro Ser Thr	
300 305 310 315	
cgg aag gac tat cct gct gcc aag agg gtc aag ttg gac agt gtc aga	1551
Arg Lys Asp Tyr Pro Ala Ala Lys Arg Val Lys Leu Asp Ser Val Arg	
320 325 330	
gtc ctg aga cag atc agc aac aac cga aaa tgc acc agc ccc agg tcc	1599
Val Leu Arg Gln Ile Ser Asn Asn Arg Lys Cys Thr Ser Pro Arg Ser	
335 340 345	
tcg gac acc gag gag aat gtc aag agg cga aca cac aac gtc ttg gag	1647
Ser Asp Thr Glu Glu Asn Val Lys Arg Arg Thr His Asn Val Leu Glu	
350 355 360	
cgc cag agg agg aac gag cta aaa cgg agc ttt ttt gcc ctg cgt gac	1695
Arg Gln Arg Arg Asn Glu Leu Lys Arg Ser Phe Phe Ala Leu Arg Asp	
365 370 375	
cag atc ccg gag ttg gaa aac aat gaa aag gcc ccc aag gta gtt atc	1743
Gln Ile Pro Glu Leu Glu Asn Asn Glu Lys Ala Pro Lys Val Val Ile	
380 385 390 395	

23/88

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ctt aaa aaa gcc aca gca tac atc ctg tcc gtc caa gca gag gag caa 1791
Leu Lys Lys Ala Thr Ala Tyr Ile Leu Ser Val Gln Ala Glu Glu Gln
      400                      405                      410

aag ctc att tct gaa gag gac ttg ttg cgg aaa cga cga gaa cag ttg 1839
Lys Leu Ile Ser Glu Glu Asp Leu Leu Arg Lys Arg Arg Glu Gln Leu
      415                      420                      425

aaa cac aaa ctt gaa cag cta cgg aac tct tgt gcg taaggaaaag 1885
Lys His Lys Leu Glu Gln Leu Arg Asn Ser Cys Ala
      430                      435

taaggaaaac gattccttct aacagaaatg tcctgagcaa tcacctatga acttggtttca 1945

aatgcatgat caaatgcaac ctcaaacct tggctgagtc ttgagactga aagatttagc 2005

cataatgtaa actgcctcaa attggacttt gggcataaaa gaactttttt atgcttacca 2065

tctttttttt ttctttaaca gatttgtatt taagaattgt ttttaaaaaa ttttaa 2121

<210> 12
<211> 2098
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (79)..(570)

<400> 12
cctgccgaag tcagttcctt gtggagccgg agctgggcgc ggattcgccg aggcaccgag 60

gcactcagag gaggcgcc atg tca gaa ccg gct ggg gat gtc cgt cag aac 111
      Met Ser Glu Pro Ala Gly Asp Val Arg Gln Asn
      1                      5                      10

cca tgc ggc agc aag gcc tgc cgc cgc ctc ttc ggc cca gtg gac agc 159
Pro Cys Gly Ser Lys Ala Cys Arg Arg Leu Phe Gly Pro Val Asp Ser
      15                      20                      25

gag cag ctg agc cgc gac tgt gat gcg cta atg gcg ggc tgc atc cag 207
Glu Gln Leu Ser Arg Asp Cys Asp Ala Leu Met Ala Gly Cys Ile Gln
      30                      35                      40

gag gcc cgt gag cga tgg aac ttc gac ttt gtc acc gag aca cca ctg 255
Glu Ala Arg Glu Arg Trp Asn Phe Asp Phe Val Thr Glu Thr Pro Leu
      45                      50                      55

gag ggt gac ttc gcc tgg gag cgt gtg cgg ggc ctt ggc ctg ccc aag 303
Glu Gly Asp Phe Ala Trp Glu Arg Val Arg Gly Leu Gly Leu Pro Lys
      60                      65                      70                      75

ctc tac ctt ccc acg ggg ccc cgg cga ggc cgg gat gag ttg gga gga 351
Leu Tyr Leu Pro Thr Gly Pro Arg Arg Gly Arg Asp Glu Leu Gly Gly
      80                      85                      90

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24/88

```

ggc agg cgg cct ggc acc tca cct gct ctg ctg cag ggg aca gca gag   399
Gly Arg Arg Pro Gly Thr Ser Pro Ala Leu Leu Gln Gly Thr Ala Glu
          95                      100                      105

gaa gac cat gtg gac ctg tca ctg tct tgt acc ctt gtg cct cgc tca   447
Glu Asp His Val Asp Leu Ser Leu Ser Cys Thr Leu Val Pro Arg Ser
          110                      115                      120

ggg gag cag gct gaa ggg tcc cca ggt gga cct gga gac tct cag ggt   495
Gly Glu Gln Ala Glu Gly Ser Pro Gly Gly Pro Gly Asp Ser Gln Gly
          125                      130                      135

cga aaa cgg cgg cag acc agc atg aca gat ttc tac cac tcc aaa cgc   543
Arg Lys Arg Arg Gln Thr Ser Met Thr Asp Phe Tyr His Ser Lys Arg
          140                      145                      150                      155

cgg ctg atc ttc tcc aag agg aag ccc taatccgccc acaggaagcc       590
Arg Leu Ile Phe Ser Lys Arg Lys Pro
          160

tgcagtcctg gaagcgcgag ggcctcaaag gcccgcctcta catcttctgc cttagtctca 650
gtttgtgtgt cttaattatt atttgtgttt taatttaaac acctcctcat gtacataccc 710
tggccgcccc ctgcccccca gcctctggca ttagaattat ttaaacaaaa actaggcggt 770
tgaatgagag gttcctaaga gtgctgggca tttttatttt atgaaatact atttaaagcc 830
tcctcatccc gtgttctcct tttcctctct cccggagggt ggggtgggccc gcttcatgcc 890
agctacttcc tctccccac ttgtccgctg ggtggtaccc tctggagggg tgtggctcct 950
tcccatcgct gtcacaggcg gttatgaaat tcacccctt tctggacac tcagacctga 1010
attctttttt atttgagaag taaacagatg gcactttgaa ggggcctcac cgagtggggg 1070
catcatcaaa aactttggag tcccctcacc tctctaaagg ttgggcaggg tgaccctgaa 1130
gtgagcacag cctagggtct agctggggac ctggtaccct cctggctctt gatacccccc 1190
tctgtcttgt gaaggcaggg ggaagggtgg gtccctggagc agaccacccc gcctgccttc 1250
atggccccctc tgacctgcac tggggagccc gtctcagtgt tgagcctttt ccctcttttg 1310
ctccccgtga ctttttgagg agccccagct acccttcttc tccagctggg ctctgcaatt 1370
cccctctgct gctgtccctc ccccttgtec tttcccttca gtaccctctc agctccaggt 1430
ggctctgagg tgctgtccc acccccaccc ccagctcaat ggactggaag gggaagggac 1490
acacaagaag aagggcaccc tagttctacc tcaggcagct caagcagcga ccgccccctc 1550
ctctagctgt gggggtgagg gtcccatgtg gtggcacagg ccccttgag tggggttatc 1610
tctgtgttag gggatatga tgggggagta gatctttcta ggaggagac actggcccct 1670
caaatcgtec agcgaccttc ctcatccacc ccatccctcc ccagttcatt gcactttgat 1730

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25/88

tagcagcggg acaaggagtc agacatttta agatggtggc agtagaggct atggacaggg 1790
catgccacgt gggctcatat ggggctggga gtagttgtct ttcttggcac taacgttgag 1850
cccttgaggg cactgaagtg cttagtgtac ttggagtatt ggggtctgac cccaaacacc 1910
ttccagctcc tgtaacatac tggcctggac tgttttctct cggtcccca tgtgtcctgg 1970
ttcccgtttc tccacctaga ctgtaaacct ctcgagggca gggaccacac cctgtactgt 2030
tctgtgtctt tcacagctcc tcccacaatg ctgatataca gcaggtgctc aataaacgat 2090
tcttagtg 2098

<210> 13
<211> 827
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (256)..(570)

<400> 13
ggcacgaggg aaagggcggc gcagcggctg ccgagctcgg ccctggaggc ggcgagaaca 60
tggtgcgag gttcttggtg accctcggga ttccggcgcg gtgcggcccg ccgcgagtga 120
gggttttctg ggttcacatc tcgtggttca cgggggagtg ggcagcgcca ggggcgcccc 180
ccgctgtggc cctcgtgctg atgctactga ggagccagcg tctagggcag cagccgcttc 240
ctagaagacc aggtc atg atg atg ggc agc gcc cga gtg gcg gag ctg ctg 291
Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu
1 5 10
ctg ctc cac ggc gcg gag ccc aac tgc gcc gac ccc gcc act ctc acc 339
Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr
15 20 25
cga ccc gtg cac gac gct gcc cgg gag ggc ttc ctg gac acg ctg gtg 387
Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val
30 35 40
gtg ctg cac cgg gcc ggg gcg cgg ctg gac gtg cgc gat gcc tgg ggc 435
Val Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly
45 50 55 60
cgt ctg ccc gtg gac ctg gct gag gag ctg ggc cat cgc gat gtc gca 483
Arg Leu Pro Val Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala
65 70 75
cgg tac ctg cgc gcg gct gcg ggg ggc acc aga ggc agt aac cat gcc 531
Arg Tyr Leu Arg Ala Ala Ala Gly Gly Thr Arg Gly Ser Asn His Ala
80 85 90

26/88

```

cgc ata gat gcc gcg gaa ggt ccc tca gac atc ccc gat tgaaagaacc      580
Arg Ile Asp Ala Ala Glu Gly Pro Ser Asp Ile Pro Asp
      95                      100                      105

agagaggctc tgagaaacct ccggaaactt agatcatcag tcaccgaagg tcctacaggg 640

ccacaactgc ccccgccaca acccaccctcg ctttcgtagt tttcatttag aaaatagagc 700

ttttaaaaat gtccctgcctt ttaacgtaga tatatgcctt cccccactac cgtaaatgtc 760

catttatatc atttttttata tattcttata aaaatgtaaa aaagaaaaaa aaaaaaaaaa 820

aaaaaaa                                           827

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<210> 14
 <211> 1275
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (163)..(681)

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<400> 14
cctccctacg ggcgccctccg gcagcccttc ccgcgtgcgc agggctcaga gccgttccga 60

gatcttggag gtccgggtgg gagtgggggt ggggtggggg tgggggtgaa ggtggggggc 120

gggcgcgctc agggaaggcg ggtgcgcgcc tgcggggcgg ag atg ggc agg ggg      174
                               Met Gly Arg Gly
                               1

cgg tgc gtg ggt ccc agt ctg cag tta agg ggg cag gag tgg cgc tgc      222
Arg Cys Val Gly Pro Ser Leu Gln Leu Arg Gly Gln Glu Trp Arg Cys
      5                      10                      15                      20

tca cct ctg gtg cca aag ggc ggc gca gcg gct gcc gag ctc ggc cct      270
Ser Pro Leu Val Pro Lys Gly Gly Ala Ala Ala Ala Glu Leu Gly Pro
      25                      30                      35

gga ggc ggc gag aac atg gtg cgc agg ttc ttg gtg acc ctc cgg att      318
Gly Gly Gly Glu Asn Met Val Arg Arg Phe Leu Val Thr Leu Arg Ile
      40                      45                      50

cgg cgc gcg tgc ggc ccg ccg cga gtg agg gtt ttc gtg gtt cac atc      366
Arg Arg Ala Cys Gly Pro Pro Arg Val Arg Val Phe Val Val His Ile
      55                      60                      65

ccg cgg ctc acg ggg gag tgg gca gcg cca ggg gcg ccc gcc gct gtg      414
Pro Arg Leu Thr Gly Glu Trp Ala Ala Pro Gly Ala Pro Ala Ala Val
      70                      75                      80

gcc ctc gtg ctg atg cta ctg agg agc cag cgt cta ggg cag cag ccg      462
Ala Leu Val Leu Met Leu Leu Arg Ser Gln Arg Leu Gly Gln Gln Pro
      85                      90                      95                      100

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27/88

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ctt cct aga aga cca ggt cat gat gat ggg cag cgc ccg agt ggc gga 510
Leu Pro Arg Arg Pro Gly His Asp Asp Gly Gln Arg Pro Ser Gly Gly
105 110 115

gct gct gct gct cca cgg cgc gga gcc caa ctg cgc cga ccc cgc cac 558
Ala Ala Ala Ala Pro Arg Arg Gly Ala Gln Leu Arg Arg Pro Arg His
120 125 130

tct cac ccg acc cgt gca cga cgc tgc ccg gga ggg ctt cct gga cac 606
Ser His Pro Thr Arg Ala Arg Arg Cys Pro Gly Gly Leu Pro Gly His
135 140 145

gct ggt ggt gct gca ccg ggc cgg ggc gcg gct gga cgt gcg cga tgc 654
Ala Gly Gly Ala Ala Pro Gly Arg Gly Ala Ala Gly Arg Ala Arg Cys
150 155 160

ctg ggg ccg tct gcc cgt gga cct ggc tgaggagctg ggccatcgcg 701
Leu Gly Pro Ser Ala Arg Gly Pro Gly
165 170

atgtcgcacg gtacctgcgc gcggctgcgg ggggcaccag aggcagtaac catgcccgca 761

tagatgccgc ggaaggtccc tcagacatcc ccgattgaaa gaaccagaga ggctctgaga 821

aacctcggga aacttagatc atcagtcacc gaaggtccta cagggccaca actgcccccg 881

ccacaaccca ccccgctttc gtagttttca tttagaaaat agagctttta aaaatgtcct 941

gcctttttaac gtagatatat gccttcccc actaccgtaa atgtccattt atatcatttt 1001

ttatatattc ttataaaaat gtaaaaaaga aaaacaccgc ttctgccttt tcaactgtgtt 1061

ggagtthttt ggagtgcgca ctcaagccct aagcgcacat tcatgtgggc atttcttgcg 1121

agcctcgcag cctccggaag ctgtcgactt catgacaagc attttgtgaa ctagggaagc 1181

tcaggggggt tactggcttc tcttgagtca cactgctagc aaatggcaga accaaagctc 1241

aaataaaaat aaaataattt tcattcatc actc 1275

<210> 15
<211> 1850
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (213)..(1616)

<400> 15
ggcccaggct gaagctcagg gccctgtctg ctctgtggac tcaacagttt gtggcaagac 60
aagctcagaa ctgagaagct gtcaccacag ttctggaggc tgggaagttc aagatcaaag 120
tgccagcaga ttcagtgtca tgtgaggacg tgttcctgc ttcatagata agagcttgga 180

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28/88

gctcggcgca caaccagcac catctggtcg	cg atg gtg gac acg gaa agc cca	233
	Met Val Asp Thr Glu Ser Pro	
	1 5	
ctc tgc ccc ctc tcc cca ctc gag gcc ggc gat cta gag agc ccg tta	281	
Leu Cys Pro Leu Ser Pro Leu Glu Ala Gly Asp Leu Glu Ser Pro Leu		
10 15 20		
tct gaa gag ttc ctg caa gaa atg gga aac atc caa gag att tcg caa	329	
Ser Glu Glu Phe Leu Gln Glu Met Gly Asn Ile Gln Glu Ile Ser Gln		
25 30 35		
tcc atc ggc gag gat agt tct gga agc ttt ggc ttt acg gaa tac cag	377	
Ser Ile Gly Glu Asp Ser Ser Gly Ser Phe Gly Phe Thr Glu Tyr Gln		
40 45 50 55		
tat tta gga agc tgt cct ggc tca gat ggc tcg gtc atc acg gac acg	425	
Tyr Leu Gly Ser Cys Pro Gly Ser Asp Gly Ser Val Ile Thr Asp Thr		
60 65 70		
ctt tca cca gct tcg agc ccc tcc tcg gtg act tat cct gtg gtc ccc	473	
Leu Ser Pro Ala Ser Ser Pro Ser Ser Val Thr Tyr Pro Val Val Pro		
75 80 85		
ggc agc gtg gac gag tct ccc agt gga gca ttg aac atc gaa tgt aga	521	
Gly Ser Val Asp Glu Ser Pro Ser Gly Ala Leu Asn Ile Glu Cys Arg		
90 95 100		
atc tgc ggg gac aag gcc tca ggc tat cat tac gga gtc cac gcg tgt	569	
Ile Cys Gly Asp Lys Ala Ser Gly Tyr His Tyr Gly Val His Ala Cys		
105 110 115		
gaa ggc tgc aag ggc ttc ttt cgg cga acg att cga ctc aag ctg gtg	617	
Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Val		
120 125 130 135		
tat gac aag tgc gac cgc agc tgc aag atc cag aaa aag aac aga aac	665	
Tyr Asp Lys Cys Asp Arg Ser Cys Lys Ile Gln Lys Lys Asn Arg Asn		
140 145 150		
aaa tgc cag tat tgt cga ttt cac aag tgc ctt tct gtc ggg atg tca	713	
Lys Cys Gln Tyr Cys Arg Phe His Lys Cys Leu Ser Val Gly Met Ser		
155 160 165		
cac aac gcg att cgt ttt gga cga atg cca aga tct gag aaa gca aaa	761	
His Asn Ala Ile Arg Phe Gly Arg Met Pro Arg Ser Glu Lys Ala Lys		
170 175 180		
ctg aaa gca gaa att ctt acc tgt gaa cat gac ata gaa gat tct gaa	809	
Leu Lys Ala Glu Ile Leu Thr Cys Glu His Asp Ile Glu Asp Ser Glu		
185 190 195		
act gca gat ctc aaa tct ctg gcc aag aga atc tac gag gcc tac ttg	857	
Thr Ala Asp Leu Lys Ser Leu Ala Lys Arg Ile Tyr Glu Ala Tyr Leu		
200 205 210 215		

29/88

aag aac ttc aac atg aac aag gtc aaa gcc cgg gtc atc ctc tca gga	905
Lys Asn Phe Asn Met Asn Lys Val Lys Ala Arg Val Ile Leu Ser Gly	
220 225 230	
aag gcc agt aac aat cca cct ttt gtc ata cat gat atg gag aca ctg	953
Lys Ala Ser Asn Asn Pro Pro Phe Val Ile His Asp Met Glu Thr Leu	
235 240 245	
tgt atg gct gag aag acg ctg gtg gcc aag ctg gtg gcc aat ggc atc	1001
Cys Met Ala Glu Lys Thr Leu Val Ala Lys Leu Val Ala Asn Gly Ile	
250 255 260	
cag aac aag gag gcg gag gtc cgc atc ttt cac tgc tgc cag tgc acg	1049
Gln Asn Lys Glu Ala Glu Val Arg Ile Phe His Cys Cys Gln Cys Thr	
265 270 275	
tca gtg gag acc gtc acg gag ctg acg gaa ttc gcc aag gcc atc cca	1097
Ser Val Glu Thr Val Thr Glu Leu Thr Glu Phe Ala Lys Ala Ile Pro	
280 285 290 295	
ggc ttc gca aac ttg gac ctg aac gat caa gtg aca ttg cta aaa tac	1145
Gly Phe Ala Asn Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr	
300 305 310	
gga gtt tat gag gcc ata ttc gcc atg ctg tct tct gtg atg aac aaa	1193
Gly Val Tyr Glu Ala Ile Phe Ala Met Leu Ser Ser Val Met Asn Lys	
315 320 325	
gac ggg atg ctg gta gcg tat gga aat ggg ttt ata act cgt gaa ttc	1241
Asp Gly Met Leu Val Ala Tyr Gly Asn Gly Phe Ile Thr Arg Glu Phe	
330 335 340	
cta aaa agc cta agg aaa ccg ttc tgt gat atc atg gaa ccc aag ttt	1289
Leu Lys Ser Leu Arg Lys Pro Phe Cys Asp Ile Met Glu Pro Lys Phe	
345 350 355	
gat ttt gcc atg aag ttc aat gca ctg gaa ctg gat gac agt gat atc	1337
Asp Phe Ala Met Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Ile	
360 365 370 375	
tcc ctt ttt gtg gct gct atc att tgc tgt gga gat cgt cct ggc ctt	1385
Ser Leu Phe Val Ala Ala Ile Ile Cys Cys Gly Asp Arg Pro Gly Leu	
380 385 390	
cta aac gta gga cac att gaa aaa atg cag gag ggt att gta cat gtg	1433
Leu Asn Val Gly His Ile Glu Lys Met Gln Glu Gly Ile Val His Val	
395 400 405	
ctc aga ctc cac ctg cag agc aac cac ccg gac gat atc ttt ctc ttc	1481
Leu Arg Leu His Leu Gln Ser Asn His Pro Asp Asp Ile Phe Leu Phe	
410 415 420	
cca aaa ctt ctt caa aaa atg gca gac ctc cgg cag ctg gtg acg gag	1529
Pro Lys Leu Leu Gln Lys Met Ala Asp Leu Arg Gln Leu Val Thr Glu	
425 430 435	

30/88

cat gcg cag ctg gtg cag atc atc aag aag acg gag tcg gat gct gcg 1577
 His Ala Gln Leu Val Gln Ile Ile Lys Lys Thr Glu Ser Asp Ala Ala
 440 445 450 455

ctg cac ccg cta ctg cag gag atc tac agg gac atg tac tgagttcctt 1626
 Leu His Pro Leu Leu Gln Glu Ile Tyr Arg Asp Met Tyr
 460 465

cagatcagcc acaccttttc caggagttct gaagctgaca gcactacaaa ggagacgggg 1686

gagcagcacg attttgcaca aatatccacc actttaacct tagagcttgg acagtctgag 1746

ctgtaggtaa ccggcatatt attccatatac tttgttttaa ccagtacttc taagagcata 1806

gaactcaaat gctgggggag gtggctaatac tcaggactgg gaag 1850

<210> 16

<211> 1609

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (92)..(1606)

<400> 16

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gaattacagc aaacccttat tccatgctgt t atg ggt gaa act ctg gga gat 112
 Met Gly Glu Thr Leu Gly Asp
 1 5

tct cct att gac cca gaa agc gat tcc ttc act gat aca ctg tct gca 160
 Ser Pro Ile Asp Pro Glu Ser Asp Ser Phe Thr Asp Thr Leu Ser Ala
 10 15 20

aac ata tca caa gaa atg acc atg gtt gac aca gag atg cca ttc tgg 208
 Asn Ile Ser Gln Glu Met Thr Met Val Asp Thr Glu Met Pro Phe Trp
 25 30 35

ccc acc aac ttt ggg atc agc tcc gtg gat ctc tcc gta atg gaa gac 256
 Pro Thr Asn Phe Gly Ile Ser Ser Val Asp Leu Ser Val Met Glu Asp
 40 45 50 55

cac tcc cac tcc ttt gat atc aag ccc ttc act act gtt gac ttc tcc 304
 His Ser His Ser Phe Asp Ile Lys Pro Phe Thr Thr Val Asp Phe Ser
 60 65 70

agc att tct act cca cat tac gaa gac att cca ttc aca aga aca gat 352
 Ser Ile Ser Thr Pro His Tyr Glu Asp Ile Pro Phe Thr Arg Thr Asp
 75 80 85

cca gtg gtt gca gat tac aag tat gac ctg aaa ctt caa gag tac caa 400
 Pro Val Val Ala Asp Tyr Lys Tyr Asp Leu Lys Leu Gln Glu Tyr Gln
 90 95 100

31/88

agt gca atc aaa gtg gag cct gca tct cca cct tat tat tct gag aag	448
Ser Ala Ile Lys Val Glu Pro Ala Ser Pro Pro Tyr Tyr Ser Glu Lys	
105 110 115	
act cag ctc tac aat aag cct cat gaa gag cct tcc aac tcc ctc atg	496
Thr Gln Leu Tyr Asn Lys Pro His Glu Glu Pro Ser Asn Ser Leu Met	
120 125 130 135	
gca att gaa tgt cgt gtc tgt gga gat aaa gct tct gga ttt cac tat	544
Ala Ile Glu Cys Arg Val Cys Gly Asp Lys Ala Ser Gly Phe His Tyr	
140 145 150	
gga gtt cat gct tgt gaa gga tgc aag ggt ttc ttc cgg aga aca atc	592
Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr Ile	
155 160 165	
aga ttg aag ctt atc tat gac aga tgt gat ctt aac tgt cgg atc cac	640
Arg Leu Lys Leu Ile Tyr Asp Arg Cys Asp Leu Asn Cys Arg Ile His	
170 175 180	
aaa aaa agt aga aat aaa tgt cag tac tgt cgg ttt cag aaa tgc ctt	688
Lys Lys Ser Arg Asn Lys Cys Gln Tyr Cys Arg Phe Gln Lys Cys Leu	
185 190 195	
gca gtg ggg atg tct cat aat gcc atc agg ttt ggg cgg atg cca cag	736
Ala Val Gly Met Ser His Asn Ala Ile Arg Phe Gly Arg Met Pro Gln	
200 205 210 215	
gcc gag aag gag aag ctg ttg gcg gag atc tcc agt gat atc gac cag	784
Ala Glu Lys Glu Lys Leu Leu Ala Glu Ile Ser Ser Asp Ile Asp Gln	
220 225 230	
ctg aat cca gag tcc gct gac ctc cgg gcc ctg gca aaa cat ttg tat	832
Leu Asn Pro Glu Ser Ala Asp Leu Arg Ala Leu Ala Lys His Leu Tyr	
235 240 245	
gac tca tac ata aag tcc ttc ccg ctg acc aaa gca aag gcg agg gcg	880
Asp Ser Tyr Ile Lys Ser Phe Pro Leu Thr Lys Ala Lys Ala Arg Ala	
250 255 260	
atc ttg aca gga aag aca aca gac aaa tca cca ttc gtt atc tat gac	928
Ile Leu Thr Gly Lys Thr Thr Asp Lys Ser Pro Phe Val Ile Tyr Asp	
265 270 275	
atg aat tcc tta atg atg gga gaa gat aaa atc aag ttc aaa cac atc	976
Met Asn Ser Leu Met Met Gly Glu Asp Lys Ile Lys Phe Lys His Ile	
280 285 290 295	
acc ccc ctg cag gag cag agc aaa gag gtg gcc atc cgc atc ttt cag	1024
Thr Pro Leu Gln Glu Gln Ser Lys Glu Val Ala Ile Arg Ile Phe Gln	
300 305 310	
ggc tgc cag ttt cgc tcc gtg gag gct gtg cag gag atc aca gag tat	1072
Gly Cys Gln Phe Arg Ser Val Glu Ala Val Gln Glu Ile Thr Glu Tyr	
315 320 325	

32/88

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gcc aaa agc att cct ggt ttt gta aat ctt gac ttg aac gac caa gta 1120
Ala Lys Ser Ile Pro Gly Phe Val Asn Leu Asp Leu Asn Asp Gln Val
      330                      335                      340

act ctc ctc aaa tat gga gtc cac gag atc att tac aca atg ctg gcc 1168
Thr Leu Leu Lys Tyr Gly Val His Glu Ile Ile Tyr Thr Met Leu Ala
      345                      350                      355

tcc ttg atg aat aaa gat ggg gtt ctc ata tcc gag ggc caa ggc ttc 1216
Ser Leu Met Asn Lys Asp Gly Val Leu Ile Ser Glu Gly Gln Gly Phe
360                      365                      370                      375

atg aca agg gag ttt cta aag agc ctg cga aag cct ttt ggt gac ttt 1264
Met Thr Arg Glu Phe Leu Lys Ser Leu Arg Lys Pro Phe Gly Asp Phe
      380                      385                      390

atg gag ccc aag ttt gag ttt gct gtg aag ttc aat gca ctg gaa tta 1312
Met Glu Pro Lys Phe Glu Phe Ala Val Lys Phe Asn Ala Leu Glu Leu
      395                      400                      405

gat gac agc gac ttg gca ata ttt att gct gtc att att ctc agt gga 1360
Asp Asp Ser Asp Leu Ala Ile Phe Ile Ala Val Ile Ile Leu Ser Gly
      410                      415                      420

gac cgc cca ggt ttg ctg aat gtg aag ccc att gaa gac att caa gac 1408
Asp Arg Pro Gly Leu Leu Asn Val Lys Pro Ile Glu Asp Ile Gln Asp
      425                      430                      435

aac ctg cta caa gcc ctg gag ctc cag ctg aag ctg aac cac cct gag 1456
Asn Leu Leu Gln Ala Leu Glu Leu Gln Leu Lys Leu Asn His Pro Glu
440                      445                      450                      455

tcc tca cag ctg ttt gcc aag ctg ctc cag aaa atg aca gac ctc aga 1504
Ser Ser Gln Leu Phe Ala Lys Leu Leu Gln Lys Met Thr Asp Leu Arg
      460                      465                      470

cag att gtc acg gaa cac gtg cag cta ctg cag gtg atc aag aag acg 1552
Gln Ile Val Thr Glu His Val Gln Leu Leu Gln Val Ile Lys Lys Thr
      475                      480                      485

gag aca gac atg agt ctt cac ccg ctc ctg cag gag atc tac aag gac 1600
Glu Thr Asp Met Ser Leu His Pro Leu Leu Gln Glu Ile Tyr Lys Asp
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ttg tac tag 1609
Leu Tyr
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<212> DNA
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33/88

<220>

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<222> (2966)..(2972)

<223> a, c, t, g, other, or unknown

<400> 17

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aagacagatg caccaacgag ggtctggaat ggtctggagt ggtctggaaa gcagggtcag 180
atacccttgg aaaactgaag cccgtggagc aatgatctct acaggactgc ttcaaggctg 240
atgggaacca ccctgtagag gtccatctgc gttcagaccc agacgatgcc agagctatga 300
ctgggcctgc aggtgtggcg ccgaggggag atcagcc atg gag cag cca cag gag 355
                               Met Glu Gln Pro Gln Glu
                               1           5

gaa gcc cct gag gtc cgg gaa gag gag gag aaa gag gaa gtg gca gag 403
Glu Ala Pro Glu Val Arg Glu Glu Glu Glu Lys Glu Glu Val Ala Glu
                               10           15           20

gca'gaa gga gcc cca gag ctc aat ggg gga cca cag cat gca ctt cct 451
Ala Glu Gly Ala Pro Glu Leu Asn Gly Gly Pro Gln His Ala Leu Pro
                               25           30           35

tcc agc agc tac aca gac ctc tcc cgg agc tcc tcg cca ccc tca ctg 499
Ser Ser Ser Tyr Thr Asp Leu Ser Arg Ser Ser Ser Pro Pro Ser Leu
                               40           45           50

ctg gac caa ctg cag atg ggc tgt gac ggg gcc tca tgc ggc agc ctc 547
Leu Asp Gln Leu Gln Met Gly Cys Asp Gly Ala Ser Cys Gly Ser Leu
                               55           60           65           70

aac atg gag tgc cgg gtg tgc ggg gac aag gca tcg ggc ttc cac tac 595
Asn Met Glu Cys Arg Val Cys Gly Asp Lys Ala Ser Gly Phe His Tyr
                               75           80           85

ggt gtt cat gca tgt gag ggg tgc aag ggc ttc ttc cgt cgt acg atc 643
Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr Ile
                               90           95           100

cgc atg aag ctg gag tac gag aag tgt gag cgc agc tgc aag att cag 691
Arg Met Lys Leu Glu Tyr Glu Lys Cys Glu Arg Ser Cys Lys Ile Gln
                               105           110           115

aag aag aac cgc aac aag tgc cag tac tgc cgc ttc cag aag tgc ctg 739
Lys Lys Asn Arg Asn Lys Cys Gln Tyr Cys Arg Phe Gln Lys Cys Leu
                               120           125           130

gca ctg ggc atg tca cac aac gct atc cgt ttt ggt cgg atg ccg gag 787
Ala Leu Gly Met Ser His Asn Ala Ile Arg Phe Gly Arg Met Pro Glu
                               135           140           145           150

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34/88

gct gag aag agg aag ctg gtg gca ggg ctg act gca aac gag ggg agc	835
Ala Glu Lys Arg Lys Leu Val Ala Gly Leu Thr Ala Asn Glu Gly Ser	
155 160 165	
cag tac aac cca cag gtg gcc gac ctg aag gcc ttc tcc aag cac atc	883
Gln Tyr Asn Pro Gln Val Ala Asp Leu Lys Ala Phe Ser Lys His Ile	
170 175 180	
tac aat gcc tac ctg aaa aac ttc aac atg acc aaa aag aag gcc cgc	931
Tyr Asn Ala Tyr Leu Lys Asn Phe Asn Met Thr Lys Lys Lys Ala Arg	
185 190 195	
agc atc ctc acc ggc aaa gcc agc cac acg gcg ccc ttt gtg atc cac	979
Ser Ile Leu Thr Gly Lys Ala Ser His Thr Ala Pro Phe Val Ile His	
200 205 210	
gac atc gag aca ttg tgg cag gca gag aag ggg ctg gtg tgg aag cag	1027
Asp Ile Glu Thr Leu Trp Gln Ala Glu Lys Gly Leu Val Trp Lys Gln	
215 220 225 230	
ttg gtg aat ggc ctg cct ccc tac aag gag atc agc gtg cac gtc ttc	1075
Leu Val Asn Gly Leu Pro Pro Tyr Lys Glu Ile Ser Val His Val Phe	
235 240 245	
tac cgc tgc cag tgc acc aca gtg gag acc gtg cgg gag ctc act gag	1123
Tyr Arg Cys Gln Cys Thr Thr Val Glu Thr Val Arg Glu Leu Thr Glu	
250 255 260	
ttc gcc aag agc atc ccc agc ttc agc agc ctc ttc ctc aac gac cag	1171
Phe Ala Lys Ser Ile Pro Ser Phe Ser Ser Leu Phe Leu Asn Asp Gln	
265 270 275	
gtt acc ctt ctc aag tat ggc gtg cac gag gcc atc ttc gcc atg ctg	1219
Val Thr Leu Leu Lys Tyr Gly Val His Glu Ala Ile Phe Ala Met Leu	
280 285 290	
gcc tct atc gtc aac aag gac ggg ctg ctg gta gcc aac ggc agt ggc	1267
Ala Ser Ile Val Asn Lys Asp Gly Leu Leu Val Ala Asn Gly Ser Gly	
295 300 305 310	
ttt gtc acc cgt gag ttc ctg cgc agc ctc cgc aaa ccc ttc agt gat	1315
Phe Val Thr Arg Glu Phe Leu Arg Ser Leu Arg Lys Pro Phe Ser Asp	
315 320 325	
atc att gag cct aag ttt gaa ttt gct gtc aag ttc aac gcc ctg gaa	1363
Ile Ile Glu Pro Lys Phe Glu Phe Ala Val Lys Phe Asn Ala Leu Glu	
330 335 340	
ctt gat gac agt gac ctg gcc cta ttc att gcg gcc atc att ctg tgt	1411
Leu Asp Asp Ser Asp Leu Ala Leu Phe Ile Ala Ala Ile Ile Leu Cys	
345 350 355	
gga gac cgg cca ggc ctc atg aac gtt cca cgg gtg gag gct atc cag	1459
Gly Asp Arg Pro Gly Leu Met Asn Val Pro Arg Val Glu Ala Ile Gln	
360 365 370	

35/88

gac acc atc ctg cgt gcc ctc gaa ttc cac ctg cag gcc aac cac cct 1507
 Asp Thr Ile Leu Arg Ala Leu Glu Phe His Leu Gln Ala Asn His Pro
 375 380 385 390

gat gcc cag tac ctc ttc ccc aag ctg ctg cag aag atg gct gac ctg 1555
 Asp Ala Gln Tyr Leu Phe Pro Lys Leu Leu Gln Lys Met Ala Asp Leu
 395 400 405

cgg caa ctg gtc acc gag cac gcc cag atg atg cag cgg atc aag aag 1603
 Arg Gln Leu Val Thr Glu His Ala Gln Met Met Gln Arg Ile Lys Lys
 410 415 420

acc gaa acc gag acc tcg ctg cac cct ctg ctc cag gag atc tac aag 1651
 Thr Glu Thr Glu Thr Ser Leu His Pro Leu Leu Gln Glu Ile Tyr Lys
 425 430 435

gac atg tac taacggcggc acccaggcct ccctgcagac tccaatgggg 1700
 Asp Met Tyr
 440

ccagcactgg agggggccac ccacatgact tttccattga ccagctctct tctgtctttt 1760
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tacagctctt	ctcagtgtct	gaacaatctc	caaaattgaa	atgtatat	ttgctaggag	3200
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ccagctcctt tcgccccgcgc cctccgttcg ctccggacac c atg gac aag ttt tgg 176
Met Asp Lys Phe Trp
 1 5

ctg agc atc gga ttt gag acc tgc agg tat ggg ttc ata gaa ggg cac 416
Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly Phe Ile Glu Gly His
70 75 80 85

37/88

gtg gtg att ccc cgg atc cac ccc aac tcc atc tgt gca gca aac aac	464
Val Val Ile Pro Arg Ile His Pro Asn Ser Ile Cys Ala Ala Asn Asn	
90 95 100	
aca ggg gtg tac atc ctc aca tcc aac acc tcc cag tat gac aca tat	512
Thr Gly Val Tyr Ile Leu Thr Ser Asn Thr Ser Gln Tyr Asp Thr Tyr	
105 110 115	
tgc ttc aat gct tca gct cca cct gaa gaa gat tgt aca tca gtc aca	560
Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp Cys Thr Ser Val Thr	
120 125 130	
gac ctg ccc aat gcc ttt gat gga cca att acc ata act att gtt aac	608
Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr Ile Thr Ile Val Asn	
135 140 145	
cgt gat ggc acc cgc tat gtc cag aaa gga gaa tac aga acg aat cct	656
Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu Tyr Arg Thr Asn Pro	
150 155 160 165	
gaa gac atc tac ccc agc aac cct act gat gat gac gtg agc agc ggc	704
Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp Asp Val Ser Ser Gly	
170 175 180	
tcc tcc agt gaa agg agc agc act tca gga ggt tac atc ttt tac acc	752
Ser Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly Tyr Ile Phe Tyr Thr	
185 190 195	
ttt tct act gta cac ccc atc cca gac gaa gac agt ccc tgg atc acc	800
Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp Ser Pro Trp Ile Thr	
200 205 210	
gac agc aca gac aga atc cct gct acc act ttg atg agc act agt gct	848
Asp Ser Thr Asp Arg Ile Pro Ala Thr Thr Leu Met Ser Thr Ser Ala	
215 220 225	
aca gca act gag aca gca acc aag agg caa gaa acc tgg gat tgg ttt	896
Thr Ala Thr Glu Thr Ala Thr Lys Arg Gln Glu Thr Trp Asp Trp Phe	
230 235 240 245	
tca tgg ttg ttt cta cca tca gag tca aag aat cat ctt cac aca aca	944
Ser Trp Leu Phe Leu Pro Ser Glu Ser Lys Asn His Leu His Thr Thr	
250 255 260	
aca caa atg gct ggt acg tct tca aat acc atc tca gca ggc tgg gag	992
Thr Gln Met Ala Gly Thr Ser Ser Asn Thr Ile Ser Ala Gly Trp Glu	
265 270 275	
cca aat gaa gaa aat gaa gat gaa aga gac aga cac ctc agt ttt tct	1040
Pro Asn Glu Glu Asn Glu Asp Glu Arg Asp Arg His Leu Ser Phe Ser	
280 285 290	
gga tca ggc att gat gat gat gaa gat ttt atc tcc agc acc att tca	1088
Gly Ser Gly Ile Asp Asp Asp Glu Asp Phe Ile Ser Ser Thr Ile Ser	
295 300 305	

38/88

acc aca cca cgg gct ttt gac cac aca aaa cag aac cag gac tgg acc	1136
Thr Thr Pro Arg Ala Phe Asp His Thr Lys Gln Asn Gln Asp Trp Thr	
310 315 320 325	
cag tgg aac cca agc cat tca aat ccg gaa gtg cta ctt cag aca acc	1184
Gln Trp Asn Pro Ser His Ser Asn Pro Glu Val Leu Leu Gln Thr Thr	
330 335 340	
aca agg atg act gat gta gac aga aat ggc acc act gct tat gaa gga	1232
Thr Arg Met Thr Asp Val Asp Arg Asn Gly Thr Thr Ala Tyr Glu Gly	
345 350 355	
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Asn Trp Asn Pro Glu Ala His Pro Pro Leu Ile His His Glu His His	
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Glu Glu Glu Glu Thr Pro His Ser Thr Ser Thr Ile Gln Ala Thr Pro	
375 380 385	
agt agt aca acg gaa gaa aca gct acc cag aag gaa cag tgg ttt ggc	1376
Ser Ser Thr Thr Glu Glu Thr Ala Thr Gln Lys Glu Gln Trp Phe Gly	
390 395 400 405	
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Asn Arg Trp His Glu Gly Tyr Arg Gln Thr Pro Lys Glu Asp Ser His	
410 415 420	
tcg aca aca ggg aca gct gca gcc tca gct cat acc agc cat cca atg	1472
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425 430 435	
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Phe Asn Pro Ile Ser His Pro Met Gly Arg Gly His Gln Ala Gly Arg	
455 460 465	
agg atg gat atg gac tcc agt cat agt ata acg ctt cag cct act gca	1616
Arg Met Asp Met Asp Ser Ser His Ser Ile Thr Leu Gln Pro Thr Ala	
470 475 480 485	
aat cca aac aca ggt ttg gtg gaa gat ttg gac agg aca gga cct ctt	1664
Asn Pro Asn Thr Gly Leu Val Glu Asp Leu Asp Arg Thr Gly Pro Leu	
490 495 500	
tca atg aca acg cag cag agt aat tct cag agc ttc tct aca tca cat	1712
Ser Met Thr Thr Gln Gln Ser Asn Ser Gln Ser Phe Ser Thr Ser His	
505 510 515	
gaa ggc ttg gaa gaa gat aaa gac cat cca aca act tct act ctg aca	1760
Glu Gly Leu Glu Glu Asp Lys Asp His Pro Thr Thr Ser Thr Leu Thr	
520 525 530	

39/88

tca agc aat agg aat gat gtc aca ggt gga aga aga gac cca aat cat	1808
Ser Ser Asn Arg Asn Asp Val Thr Gly Gly Arg Arg Asp Pro Asn His	
535 540 545	
tct gaa ggc tca act act tta ctg gaa ggt tat acc tct cat tac cca	1856
Ser Glu Gly Ser Thr Thr Leu Leu Glu Gly Tyr Thr Ser His Tyr Pro	
550 555 560 565	
cac acg aag gaa agc agg acc ttc atc cca gtg acc tca gct aag act	1904
His Thr Lys Glu Ser Arg Thr Phe Ile Pro Val Thr Ser Ala Lys Thr	
570 575 580	
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Gly Ser Phe Gly Val Thr Ala Val Thr Val Gly Asp Ser Asn Ser Asn	
585 590 595	
gtc aat cgt tcc tta tca gga gac caa gac aca ttc cac ccc agt ggg	2000
Val Asn Arg Ser Leu Ser Gly Asp Gln Asp Thr Phe His Pro Ser Gly	
600 605 610	
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Gly Ser His Thr Thr His Gly Ser Glu Ser Asp Gly His Ser His Gly	
615 620 625	
agt caa gaa ggt gga gca aac aca acc tct ggt cct ata agg aca ccc	2096
Ser Gln Glu Gly Gly Ala Asn Thr Thr Ser Gly Pro Ile Arg Thr Pro	
630 635 640 645	
caa att cca gaa tgg ctg atc atc ttg gca tcc ctc ttg gcc ttg gct	2144
Gln Ile Pro Glu Trp Leu Ile Ile Leu Ala Ser Leu Leu Ala Leu Ala	
650 655 660	
ttg att ctt gca gtt tgc att gca gtc aac agt cga aga agg tgt ggg	2192
Leu Ile Leu Ala Val Cys Ile Ala Val Asn Ser Arg Arg Arg Cys Gly	
665 670 675	
cag aag aaa aag cta gtg atc aac agt ggc aat gga gct gtg gag gac	2240
Gln Lys Lys Lys Leu Val Ile Asn Ser Gly Asn Gly Ala Val Glu Asp	
680 685 690	
aga aag cca agt gga ctc aac gga gag gcc agc aag tct cag gaa atg	2288
Arg Lys Pro Ser Gly Leu Asn Gly Glu Ala Ser Lys Ser Gln Glu Met	
695 700 705	
gtg cat ttg gtg aac aag gag tcg tca gaa act cca gac cag ttt atg	2336
Val His Leu Val Asn Lys Glu Ser Ser Glu Thr Pro Asp Gln Phe Met	
710 715 720 725	
aca gct gat gag aca agg aac ctg cag aat gtg gac atg aag att ggg	2384
Thr Ala Asp Glu Thr Arg Asn Leu Gln Asn Val Asp Met Lys Ile Gly	
730 735 740	
gtg taacacctac accattatct tggaagaaa caaccgttg aaacataacc	2437
Val	
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cttttttagc ataaaatttt ctactctttt tgttttttgt gttttgttct ttaaagtcag	2557

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ccctggatca	gtcctttgat	cagtataatt	ttttaaagtt	actttgtcag	aggcacaaaa	3037
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attccggccc caactgcacc atccctggcc tgtggacctg gctccggaat tcaactgcggc 240
ccagccccc cttcaccac ttccctgctca ctcacgggcg ctggttcttg gagtttgtca 300
atgccacctt catccgagag atg ctc atg cgc ctg gta ctc aca gtg cgc tcc 353
Met Leu Met Arg Leu Val Leu Thr Val Arg Ser
1 5 10
aac ctt atc ccc agt ccc ccc acc tac aac tca gca cat gac tac atc 401
Asn Leu Ile Pro Ser Pro Pro Thr Tyr Asn Ser Ala His Asp Tyr Ile
15 20 25
agc tgg gag tct ttc tcc aac gtg agc tat tac act cgt att ctg ccc 449
Ser Trp Glu Ser Phe Ser Asn Val Ser Tyr Tyr Thr Arg Ile Leu Pro
30 35 40
tct gtg cct aaa gat tgc ccc aca ccc atg gga acc aaa ggg aag aag 497
Ser Val Pro Lys Asp Cys Pro Thr Pro Met Gly Thr Lys Gly Lys Lys
45 50 55

```

41/88

cag ttg cca gat gcc cag ctc ctg gcc cgc cgc ttc ctg ctc agg agg	545
Gln Leu Pro Asp Ala Gln Leu Leu Ala Arg Arg Phe Leu Leu Arg Arg	
60 65 70 75	
aag ttc ata cct gac ccc caa ggc acc aac ctc atg ttt gcc ttc ttt	593
Lys Phe Ile Pro Asp Pro Gln Gly Thr Asn Leu Met Phe Ala Phe Phe	
80 85 90	
gca caa cac ttc acc cac cag ttc ttc aaa act tct ggc aag atg ggt	641
Ala Gln His Phe Thr His Gln Phe Phe Lys Thr Ser Gly Lys Met Gly	
95 100 105	
cct ggc ttc acc aag gcc ttg ggc cat ggg gta gac ctc ggc cac att	689
Pro Gly Phe Thr Lys Ala Leu Gly His Gly Val Asp Leu Gly His Ile	
110 115 120	
tat gga gac aat ctg gag cgt cag tat caa ctg cgg ctc ttt aag gat	737
Tyr Gly Asp Asn Leu Glu Arg Gln Tyr Gln Leu Arg Leu Phe Lys Asp	
125 130 135	
ggg aaa ctc aag tac cag gtg ctg gat gga gaa atg tac ccg ccc tcg	785
Gly Lys Leu Lys Tyr Gln Val Leu Asp Gly Glu Met Tyr Pro Pro Ser	
140 145 150 155	
gta gaa gag gcg cct gtg ttg atg cac tac ccc cga ggc atc ccg ccc	833
Val Glu Glu Ala Pro Val Leu Met His Tyr Pro Arg Gly Ile Pro Pro	
160 165 170	
cag agc cag atg gct gtg ggc cag gag gtg ttt ggg ctg ctt cct ggg	881
Gln Ser Gln Met Ala Val Gly Gln Glu Val Phe Gly Leu Leu Pro Gly	
175 180 185	
ctc atg ctg tat gcc acg ctc tgg cta cgt gag cac aac cgt gtg tgt	929
Leu Met Leu Tyr Ala Thr Leu Trp Leu Arg Glu His Asn Arg Val Cys	
190 195 200	
gac ctg ctg aag gct gag cac ccc acc tgg ggc gat gag cag ctt ttc	977
Asp Leu Leu Lys Ala Glu His Pro Thr Trp Gly Asp Glu Gln Leu Phe	
205 210 215	
cag acg acc cgc ctc atc ctc ata ggg gag acc atc aag att gtc atc	1025
Gln Thr Thr Arg Leu Ile Leu Ile Gly Glu Thr Ile Lys Ile Val Ile	
220 225 230 235	
gag gag tac gtg cag cag ctg agt ggc tat ttc ctg cag ctg aaa ttt	1073
Glu Glu Tyr Val Gln Gln Leu Ser Gly Tyr Phe Leu Gln Leu Lys Phe	
240 245 250	
gac cca gag ctg ctg ttc ggt gtc cag ttc caa tac cgc aac cgc att	1121
Asp Pro Glu Leu Leu Phe Gly Val Gln Phe Gln Tyr Arg Asn Arg Ile	
255 260 265	
gcc atg gag ttc aac cat ctc tac cac tgg cac ccc ctc atg cct gac	1169
Ala Met Glu Phe Asn His Leu Tyr His Trp His Pro Leu Met Pro Asp	
270 275 280	

42/88

tcc ttc aag gtg ggc tcc cag gag tac agc tac gag cag ttc ttg ttc	1217
Ser Phe Lys Val Gly Ser Gln Glu Tyr Ser Tyr Glu Gln Phe Leu Phe	
285 290 295	
aac acc tcc atg ttg gtg gac tat ggg gtt gag gcc ctg gtg gat gcc	1265
Asn Thr Ser Met Leu Val Asp Tyr Gly Val Glu Ala Leu Val Asp Ala	
300 305 310 315	
ttc tct cgc cag att gct ggc cgg atc ggt ggg ggc agg aac atg gac	1313
Phe Ser Arg Gln Ile Ala Gly Arg Ile Gly Gly Gly Arg Asn Met Asp	
320 325 330	
cac cac atc ctg cat gtg gct gtg gat gtc atc agg gag tct cgg gag	1361
His His Ile Leu His Val Ala Val Asp Val Ile Arg Glu Ser Arg Glu	
335 340 345	
atg cgg ctg cag ccc ttc aat gag tac cgc aag agg ttt ggc atg aaa	1409
Met Arg Leu Gln Pro Phe Asn Glu Tyr Arg Lys Arg Phe Gly Met Lys	
350 355 360	
ccc tac acc tcc ttc cag gag ctc gta gga gag aag gag atg gca gca	1457
Pro Tyr Thr Ser Phe Gln Glu Leu Val Gly Glu Lys Glu Met Ala Ala	
365 370 375	
gag ttg gag gaa ttg tat gga gac att gat gcg ttg gag ttc tac cct	1505
Glu Leu Glu Glu Leu Tyr Gly Asp Ile Asp Ala Leu Glu Phe Tyr Pro	
380 385 390 395	
gga ctg ctt ctt gaa aag tgc cat cca aac tct atc ttt ggg gag agt	1553
Gly Leu Leu Leu Glu Lys Cys His Pro Asn Ser Ile Phe Gly Glu Ser	
400 405 410	
atg ata gag att ggg gct ccc ttt tcc ctc aag ggt ctc cta ggg aat	1601
Met Ile Glu Ile Gly Ala Pro Phe Ser Leu Lys Gly Leu Leu Gly Asn	
415 420 425	
ccc atc tgt tct ccg gag tac tgg aag ccg agc aca ttt ggc ggc gag	1649
Pro Ile Cys Ser Pro Glu Tyr Trp Lys Pro Ser Thr Phe Gly Gly Glu	
430 435 440	
gtg ggc ttt aac att gtc aag acg gcc aca ctg aag aag ctg gtc tgc	1697
Val Gly Phe Asn Ile Val Lys Thr Ala Thr Leu Lys Lys Leu Val Cys	
445 450 455	
ctc aac acc aag acc tgt ccc tac gtt tcc ttc cgt gtg ccg gat gcc	1745
Leu Asn Thr Lys Thr Cys Pro Tyr Val Ser Phe Arg Val Pro Asp Ala	
460 465 470 475	
agt cag gat gat ggg cct gct gtg gag cga cca tcc aca gag	1787
Ser Gln Asp Asp Gly Pro Ala Val Glu Arg Pro Ser Thr Glu	
480 485	
ctctgagggg caggaaagca gcattctgga ggggagagct ttgtgcttgt cattccagag	1847
tgctgaggcc agggctgatg gtcttaaagt ctcattttct gggttgcat ggtgagtgtt	1907
ggggttgaca tttagaactt taagtctcac ccattatctg gaatattgtg attctgttta	1967

ttcttccaga	atgctgaact	ccttgttagc	ccttcagatt	gttaggagt	gttctcattt	2027
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tgtaacacag	tcattctagg	atgtggagct	actgatgaaa	tctgctagaa	agttaggggg	2147
ttcttatttt	gcattccaga	atcttgactt	tctgattgg	gattcaaagt	gttgtgttcc	2207
tggctgatga	tccagaacag	tggctcgtat	cccaaactctg	tcagcatctg	gctgtctaga	2267
atgtggattt	gattcatttt	cctgttcagt	gagatatcat	agagacggag	atcctaaggt	2327
ccaacaagaa	tgcattccct	gaatctgtgc	ctgcactgag	agggcaagga	agtgggggtg	2387
tcttcttggg	acccccacta	agaccctggt	ctgaggatgt	agagagaaca	ggtgggctgt	2447
attcacgcca	ttggttgga	gctaccagag	ctctatcccc	atccaggctct	tgactcatgg	2507
cagctgtttc	tcatgaagct	aataaaattc	gc			2539

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<220>
<221> CDS
<222> (232) .. (519)
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aag gga agc aaa aac aag ggt gct gcc aag acc cgg aaa acc acc aca 429
Lys Gly Ser Lys Asn Lys Gly Ala Ala Lys Thr Arg Lys Thr Thr Thr
55 60 65

44/88

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act cca gga agg aaa cca agg ggc aga ccc aaa aaa ctg gag aag gag 477
Thr Pro Gly Arg Lys Pro Arg Gly Arg Pro Lys Lys Leu Glu Lys Glu
          70                      75                      80

gaa gag gag ggc atc tcg cag gag tcc tcg gag gag gag cag 519
Glu Glu Glu Gly Ile Ser Gln Glu Ser Ser Glu Glu Glu Gln
          85                      90                      95

tgacccatgc gtgccgcctg ctctcactg gaggagcagc ttccttctgg gactggacag 579

ctttgtctccg ctcccaccgc ccccgccctt tcccaggcc caccatcacc accgcctctg 639

gccgccaccc ccatcttcca cctgtgccct caccaccaca ctacacagca caccagccgc 699

tgcagggtctc coatgggctg agtggggagc agttttcccc tggcctcagt tcccagctcc 759

ccccgcccac ccacgcatac acacatgccc tcctggacaa ggctaacatc ccacttagcc 819

gcacctgca cctgctgcgt ccccactccc ttggtggtgg ggacattgct ctctgggctt 879

ttggtttggg ggcgcctct ctgcctcctt cactgttccc tctggcttcc catagtgggg 939

cctgggaggg ttccccctgg ccttaaaagg ggcccaagcc catctcatcc tggcacgccc 999

tactccactg ccctggcagc agcaggtgtg gccaatggag gggggtgctg gccccagga 1059

ttcccccagc caaactgtct ttgtcaccac gtggggctca cttttcatcc ttccccaaact 1119

tcctagtcc ccgtactagg ttggacagcc cccttcggct acaggaaggc aggagggtg 1179

agtccctac tccctcttca ctgtggccac agcccccttg ccctccgcct gggatctgag 1239

tacatatgt ggtgatggag atgcagtcac ttattgtcca ggtgaggccc aagagccctg 1299

tggccgccac ctgaggtggg ctggggctgc tcccctaacc ctactttgct tccgccactc 1359

agccatttcc ccctcctcag atggggcacc aataacaagg agctcacctt gcccgctccc 1419

aacccccctc ctgctcctcc ctgcccccca aggttctggt tccatttttc ctctgttcac 1479

aaactacctc tggacagtgt tgttggtttt tgttcaatgt tccattcttc gacatccgtc 1539

attgctgctg ctaccagcgc caaatgttca tcctcattgc ctctgttct gccacgatac 1599

ccctccccca agatactctt tgtggggaag aggggtggtg gcatggcagg ctgggtgacc 1659

gactacccca gtcccaggga aggtgccctg cccctaggat gctgcagcag agtgagcaag 1719

ggggcccgaa tcgaccataa aggggtgtagg ggccacctcc tccccctgtt ctgttgggga 1779

ggggtagcca tgatttgtcc cagcctgggg ctccctctct ggtttcctat ttacagttac 1839

ttgaataaaa aaaatatact tttctggaaa aaaaaa 1875

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<211> 626
<212> DNA
<213> Homo sapiens
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cgctctcgtt tcattttctg cagcgcgcca cgagg atg gcc cac aag cag atc      113  
                               Met Ala His Lys Gln Ile  
                                1              5  
  
tac tac tcg gac aag tac ttc gac gaa cac tac gag tac cgg cat gtt     161  
Tyr Tyr Ser Asp Lys Tyr Phe Asp Glu His Tyr Glu Tyr Arg His Val  
                        10                  15                20  
  
atg tta ccc aga gaa ctt tcc aaa caa gta cct aaa act cat ctg atg    209  
Met Leu Pro Arg Glu Leu Ser Lys Gln Val Pro Lys Thr His Leu Met  
             25                 30               35  
  
tgt gaa gag gag tgg agg aga ctt ggt gtc caa cag agt cta ggc tgg     257  
Ser Glu Glu Glu Trp Arg Arg Leu Gly Val Gln Gln Ser Leu Gly Trp  
        40                      45                   50  
  
gtt cat tac atg att cat gag cca gaa cca cat att ctt ctc ttt aga    305  
Val His Tyr Met Ile His Glu Pro Glu Pro His Ile Leu Leu Phe Arg  
   55                     60                       65           70  
  
cga cct ctt cca aaa gat caa caa aaa tgaagtttat ctgggggatcg       352  
Arg Pro Leu Pro Lys Asp Gln Gln Lys  
                    75  
  
tcaaatacttt ttcaaattaa atgtatatgt gtatataagg tagtattcag tgaataacttg 412  
  
agaaatgtac aaatcttttca tccataacctg tgcatgagct gtattcttca cagcaacaga 472  
  
gctcagttaa atgcaactgc aagtaggcta ctgtaaatg ttaaagataa aagttcttcc 532  
  
agtcagtttt tctcttaagt gcctgtttga gtttactgaa acagtgttact tttgttcaat 592  
  
aaagtttgta tggtgcattt aaaaaaaaaa aaaa                             626
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<210> 22
<211> 3480
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (268) .. (2922)
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46/88

<400> 22

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tccgtcccgt ccaccgtccg cagctggtag ccagcctgcc cctcgccctcg actccctttc 120
accaacaccg acacccacat tgacacctcc agtcgggcca gccgctccac tcgttgccctt 180
tgcattctcca cacatggcgt cctcgcgagc agcggcggtt cctccggggg acccgcggtc 240
cccaccgtgc agcggggcat catcaag atg gtc ctc tca ggg tgc gcc atc att 294
Met Val Leu Ser Gly Cys Ala Ile Ile
1 5

gtc cga ggt cag cct cgt ggt ggg cct cct cct gag cgg cag atc aac 342
Val Arg Gly Gln Pro Arg Gly Gly Pro Pro Pro Glu Arg Gln Ile Asn
10 15 20 25

ctc agc aac att cgt gct gga aat ctt gct cgc cgg gca gcc gcc aca 390
Leu Ser Asn Ile Arg Ala Gly Asn Leu Ala Arg Arg Ala Ala Ala Thr
30 35 40

caa cct gat gca aag gat acc cct gat gag ccc tgg gca ttt cca gct 438
Gln Pro Asp Ala Lys Asp Thr Pro Asp Glu Pro Trp Ala Phe Pro Ala
45 50 55

cga gag ttc ctt cga aag aag ctg att ggg aag gaa gtc tgt ttc acg 486
Arg Glu Phe Leu Arg Lys Lys Leu Ile Gly Lys Glu Val Cys Phe Thr
60 65 70

ata gaa aac aag act ccc cag ggg cga gag tat ggc atg atc tac ctt 534
Ile Glu Asn Lys Thr Pro Gln Gly Arg Glu Tyr Gly Met Ile Tyr Leu
75 80 85

gga aaa gat acc aat ggg gaa aac att gca gaa tca ctg gtt gca gag 582
Gly Lys Asp Thr Asn Gly Glu Asn Ile Ala Glu Ser Leu Val Ala Glu
90 95 100 105

ggc tta gcc acc cgg aga gaa ggc atg aga gct aat aat cct gag cag 630
Gly Leu Ala Thr Arg Arg Glu Gly Met Arg Ala Asn Asn Pro Glu Gln
110 115 120

aac cgg ctt tca gaa tgt gaa gaa caa gca aag gca gcc aag aaa ggg 678
Asn Arg Leu Ser Glu Cys Glu Glu Gln Ala Lys Ala Ala Lys Lys Gly
125 130 135

atg tgg agt gag ggg aac ggt tca cat act atc cgg gat ctc aag tat 726
Met Trp Ser Glu Gly Asn Gly Ser His Thr Ile Arg Asp Leu Lys Tyr
140 145 150

acc att gaa aac cca agg cac ttt gtg gac tca cac cac cag aag cct 774
Thr Ile Glu Asn Pro Arg His Phe Val Asp Ser His His Gln Lys Pro
155 160 165

gtt aat gct atc atc gag cat gtg cgg gac ggc agt gtg gtc agg gcc 822
Val Asn Ala Ile Ile Glu His Val Arg Asp Gly Ser Val Val Arg Ala
170 175 180 185

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47/88

ctg ctc ctc cca gat tac tac ctg gtt aca gtc atg ctg tca ggc atc	870
Leu Leu Leu Pro Asp Tyr Tyr Leu Val Thr Val Met Leu Ser Gly Ile	
190 195 200	
aag tgc cca act ttt cga cgg gaa gca gat ggc agt gaa act cca gag	918
Lys Cys Pro Thr Phe Arg Arg Glu Ala Asp Gly Ser Glu Thr Pro Glu	
205 210 215	
cct ttt gct gca gaa gcc aaa ttt ttc act gag tcg cga ctg ctt cag	966
Pro Phe Ala Ala Glu Ala Lys Phe Phe Thr Glu Ser Arg Leu Leu Gln	
220 225 230	
aga gat gtt cag atc att ctg gag agc tgc cac aac cag aac att gtg	1014
Arg Asp Val Gln Ile Ile Leu Glu Ser Cys His Asn Gln Asn Ile Val	
235 240 245	
ggc acc atc ctt cat cca aat ggc aac atc aca gag ctc ctc ctg aag	1062
Gly Thr Ile Leu His Pro Asn Gly Asn Ile Thr Glu Leu Leu Lys	
250 255 260 265	
gaa ggt ttc gca cgc tgt gtg gac tgg tcg att gca gtt tac acc cgg	1110
Glu Gly Phe Ala Arg Cys Val Asp Trp Ser Ile Ala Val Tyr Thr Arg	
270 275 280	
ggc gca gaa aag ctg agg gcg gca gag agg ttt gcc aaa gag cgc agg	1158
Gly Ala Glu Lys Leu Arg Ala Ala Glu Arg Phe Ala Lys Glu Arg Arg	
285 290 295	
ctg aga ata tgg aga gac tat gtg gct ccc aca gct aat ttg gac caa	1206
Leu Arg Ile Trp Arg Asp Tyr Val Ala Pro Thr Ala Asn Leu Asp Gln	
300 305 310	
aag gac aag cag ttt gtt gcc aag gtg atg cag gtt ctg aat gct gat	1254
Lys Asp Lys Gln Phe Val Ala Lys Val Met Gln Val Leu Asn Ala Asp	
315 320 325	
gcc att gtt gtg aag ctg aac tca ggc gat tac aag acg att cac ctg	1302
Ala Ile Val Val Lys Leu Asn Ser Gly Asp Tyr Lys Thr Ile His Leu	
330 335 340 345	
tcc agc atc cga cca ccg agg ctg gag ggg gag aac acc cag gat aag	1350
Ser Ser Ile Arg Pro Pro Arg Leu Glu Gly Glu Asn Thr Gln Asp Lys	
350 355 360	
aac aag aaa ctg cgt ccc ctg tat gac att cct tac atg ttt gag gcc	1398
Asn Lys Lys Leu Arg Pro Leu Tyr Asp Ile Pro Tyr Met Phe Glu Ala	
365 370 375	
cgg gaa ttt ctt cga aaa aag ctt att ggg aag aag gtc aat gtg acg	1446
Arg Glu Phe Leu Arg Lys Lys Leu Ile Gly Lys Lys Val Asn Val Thr	
380 385 390	
gtg gac tac att aga cca gcc agc cca gcc aca gag aca gtg cct gcc	1494
Val Asp Tyr Ile Arg Pro Ala Ser Pro Ala Thr Glu Thr Val Pro Ala	
395 400 405	

48/88

ttt tca gag cgt acc tgt gcc act gtc acc att gga gga ata aac att	1542
Phe Ser Glu Arg Thr Cys Ala Thr Val Thr Ile Gly Gly Ile Asn Ile	
410 415 420 425	
gct gag gct ctt gtc agc aaa ggt cta gcc aca gtg atc aga tac cgg	1590
Ala Glu Ala Leu Val Ser Lys Gly Leu Ala Thr Val Ile Arg Tyr Arg	
430 435 440	
cag gat gat gac cag aga tca tca cac tac gat gaa ctg ctt gct gca	1638
Gln Asp Asp Asp Gln Arg Ser Ser His Tyr Asp Glu Leu Leu Ala Ala	
445 450 455	
gag gcc aga gct att aag aat ggc aaa gga ttg cat agc aag aag gaa	1686
Glu Ala Arg Ala Ile Lys Asn Gly Lys Gly Leu His Ser Lys Lys Glu	
460 465 470	
gtg cct atc cac cgt gtt gca gat ata tct ggg gat acc caa aaa gca	1734
Val Pro Ile His Arg Val Ala Asp Ile Ser Gly Asp Thr Gln Lys Ala	
475 480 485	
aag cag ttc ctg cct ttt ctt cag cgg gca ggt cgt tct gaa gct gtg	1782
Lys Gln Phe Leu Pro Phe Leu Gln Arg Ala Gly Arg Ser Glu Ala Val	
490 495 500 505	
gtg gaa tac gtc ttc agt ggt tct cgt ctc aaa ctc tat ttg cca aag	1830
Val Glu Tyr Val Phe Ser Gly Ser Arg Leu Lys Leu Tyr Leu Pro Lys	
510 515 520	
gaa act tgc ctt atc acc ttc ttg ctt gca ggc att gaa tgc ccc aga	1878
Glu Thr Cys Leu Ile Thr Phe Leu Leu Ala Gly Ile Glu Cys Pro Arg	
525 530 535	
gga gcc cga aac ctc cca ggc ttg gtg cag gaa gga gag ccc ttc agc	1926
Gly Ala Arg Asn Leu Pro Gly Leu Val Gln Glu Gly Glu Pro Phe Ser	
540 545 550	
gag gaa gct aca ctt ttc acc aag gaa ctg gtg ctg cag cga gag gtg	1974
Glu Glu Ala Thr Leu Phe Thr Lys Glu Leu Val Leu Gln Arg Glu Val	
555 560 565	
gag gtg gag gtg gag agc atg gac aag gcc ggc aac ttt atc ggc tgg	2022
Glu Val Glu Val Glu Ser Met Asp Lys Ala Gly Asn Phe Ile Gly Trp	
570 575 580 585	
ctg cac atc gac ggt gcc aac ctg tcc gtc ctg ctg gtg gag cac gcg	2070
Leu His Ile Asp Gly Ala Asn Leu Ser Val Leu Leu Val Glu His Ala	
590 595 600	
ctc tcc aag gtc cac ttc acc gcc gaa cgc agc tcc tac tac aag tcc	2118
Leu Ser Lys Val His Phe Thr Ala Glu Arg Ser Ser Tyr Tyr Lys Ser	
605 610 615	
ctg ctg tct gcc gag gag gcc gca aag cag aag aaa gag aag gtc tgg	2166
Leu Leu Ser Ala Glu Glu Ala Ala Lys Gln Lys Lys Glu Lys Val Trp	
620 625 630	

49/88

gcc cac tat gag gag cag ccc gtg gag gag gtg atg cca gtg ctg gag	2214
Ala His Tyr Glu Glu Gln Pro Val Glu Glu Val Met Pro Val Leu Glu	
635 640 645	
 gag aag gag cga tct gct agc tac aag ccc gtg ttt gtg acc gag atc	2262
Glu Lys Glu Arg Ser Ala Ser Tyr Lys Pro Val Phe Val Thr Glu Ile	
650 655 660 665	
 act gat gac ctg cac ttc tac gtg cag gat gtg gag acc ggc acc cag	2310
Thr Asp Asp Leu His Phe Tyr Val Gln Asp Val Glu Thr Gly Thr Gln	
670 675 680	
 ttc cag aag ctg atg gag aac atg cgc aat gac att gcc agt cac ccc	2358
Phe Gln Lys Leu Met Glu Asn Met Arg Asn Asp Ile Ala Ser His Pro	
685 690 695	
 cct gta gag ggc tcc tat gcc ccc cgc agg gga gag ttc tgc att gcc	2406
Pro Val Glu Gly Ser Tyr Ala Pro Arg Arg Gly Glu Phe Cys Ile Ala	
700 705 710	
 aaa ttt gta gat gga gaa tgg tac cgt gcc cga gta gag aaa gtc gag	2454
Lys Phe Val Asp Gly Glu Trp Tyr Arg Ala Arg Val Glu Lys Val Glu	
715 720 725	
 tct cct gcc aaa ata cat gtc ttc tac att gac tac ggc aac aga gag	2502
Ser Pro Ala Lys Ile His Val Phe Tyr Ile Asp Tyr Gly Asn Arg Glu	
730 735 740 745	
 gtc ctg cca tcc acc cgc ctg ggt acc cta tca cct gcc ttc agc act	2550
Val Leu Pro Ser Thr Arg Leu Gly Thr Leu Ser Pro Ala Phe Ser Thr	
750 755 760	
 cgg gtg ctg cca gct caa gcc acg gag tat gcc ttc gcc ttc atc cag	2598
Arg Val Leu Pro Ala Gln Ala Thr Glu Tyr Ala Phe Ala Phe Ile Gln	
765 770 775	
 gtg ccc caa gat gat gat gcc cgc acg gac gcc gtg gac agc gta gtt	2646
Val Pro Gln Asp Asp Asp Ala Arg Thr Asp Ala Val Asp Ser Val Val	
780 785 790	
 cgg gat atc cag aac act cag tgc ctg ctc aac gtg gaa cac ctg agt	2694
Arg Asp Ile Gln Asn Thr Gln Cys Leu Leu Asn Val Glu His Leu Ser	
795 800 805	
 gcc ggc tgc ccc cat gtc acc ctg cag ttt gca gat tcc aag ggc gat	2742
Ala Gly Cys Pro His Val Thr Leu Gln Phe Ala Asp Ser Lys Gly Asp	
810 815 820 825	
 gtg ggg ctg ggc ttg gtg aag gaa ggg ctg gtc atg gtg gag gtg cgc	2790
Val Gly Leu Gly Leu Val Lys Glu Gly Leu Val Met Val Glu Val Arg	
830 835 840	
 aag gag aaa cag ttc cag aaa gtg atc aca gaa tac ctg aat gcc caa	2838
Lys Glu Lys Gln Phe Gln Lys Val Ile Thr Glu Tyr Leu Asn Ala Gln	
845 850 855	

50/88

gag tca gcc aag agc gcc agg ctg aac ctg tgg cgc tat gga gac ttt 2886
 Glu Ser Ala Lys Ser Ala Arg Leu Asn Leu Trp Arg Tyr Gly Asp Phe
 860 865 870

 cga gct gat gat gca gac gaa ttt ggc tac agc cgc taaggagggg 2932
 Arg Ala Asp Asp Ala Asp Glu Phe Gly Tyr Ser Arg
 875 880 885

 atcggggtttg gccccagcc cccgtcacgc cagtccctct tcctctgccg ggaggggtgtt 2992
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 tctgatacgt ccattctcaa atgccagtgt gttcacatct tcgctctggc cagcccatte 3412
 tgtatttaaa gctttttgag gccaataaa atagtacgtg ctgctgcagc ccttattgat 3472
 caaaaaaa 3480

<210> 23
 <211> 67
 <212> PRT
 <213> Homo sapiens

<400> 23
 Met Thr Ser Lys Leu Ala Val Ala Leu Leu Ala Ala Phe Leu Ile Ser
 1 5 10 15
 Ala Ala Leu Cys Glu Gly Ala Val Leu Pro Arg Ser Ala Lys Glu Leu
 20 25 30
 Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro Phe His Pro Lys Phe
 35 40 45
 Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His Cys Ala Asn Thr
 50 55 60
 Glu Ile Met
 65

<210> 24
 <211> 604
 <212> PRT
 <213> Homo sapiens

51/88

<400> 24

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Met Leu Ala Arg Ala Leu Leu Leu Cys Ala Val Leu Ala Leu Ser His
 1              5              10              15

Thr Ala Asn Pro Cys Cys Ser His Pro Cys Gln Asn Arg Gly Val Cys
      20              25              30

Met Ser Val Gly Phe Asp Gln Tyr Lys Cys Asp Cys Thr Arg Thr Gly
      35              40              45

Phe Tyr Gly Glu Asn Cys Ser Thr Pro Glu Phe Leu Thr Arg Ile Lys
      50              55              60

Leu Phe Leu Lys Pro Thr Pro Asn Thr Val His Tyr Ile Leu Thr His
      65              70              75              80

Phe Lys Gly Phe Trp Asn Val Val Asn Asn Ile Pro Phe Leu Arg Asn
      85              90              95

Ala Ile Met Ser Tyr Val Leu Thr Ser Arg Ser His Leu Ile Asp Ser
      100              105              110

Pro Pro Thr Tyr Asn Ala Asp Tyr Gly Tyr Lys Ser Trp Glu Ala Phe
      115              120              125

Ser Asn Leu Ser Tyr Tyr Thr Arg Ala Leu Pro Pro Val Pro Asp Asp
      130              135              140

Cys Pro Thr Pro Leu Gly Val Lys Gly Lys Lys Gln Leu Pro Asp Ser
      145              150              155              160

Asn Glu Ile Val Glu Lys Leu Leu Leu Arg Arg Lys Phe Ile Pro Asp
      165              170              175

Pro Gln Gly Ser Asn Met Met Phe Ala Phe Phe Ala Gln His Phe Thr
      180              185              190

His Gln Phe Phe Lys Thr Asp His Lys Arg Gly Pro Ala Phe Thr Asn
      195              200              205

Gly Leu Gly His Gly Val Asp Leu Asn His Ile Tyr Gly Glu Thr Leu
      210              215              220

Ala Arg Gln Arg Lys Leu Arg Leu Phe Lys Asp Gly Lys Met Lys Tyr
      225              230              235              240

Gln Ile Ile Asp Gly Glu Met Tyr Pro Pro Thr Val Lys Asp Thr Gln
      245              250              255

Ala Glu Met Ile Tyr Pro Pro Gln Val Pro Glu His Leu Arg Phe Ala
      260              265              270

Val Gly Gln Glu Val Phe Gly Leu Val Pro Gly Leu Met Met Tyr Ala
      275              280              285

Thr Ile Trp Leu Arg Glu His Asn Arg Val Cys Asp Val Leu Lys Gln
      290              295              300

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52/88

Glu His Pro Glu Trp Gly Asp Glu Gln Leu Phe Gln Thr Ser Arg Leu
 305 310 315 320
 Ile Leu Ile Gly Glu Thr Ile Lys Ile Val Ile Glu Asp Tyr Val Gln
 325 330 335
 His Leu Ser Gly Tyr His Phe Lys Leu Lys Phe Asp Pro Glu Leu Leu
 340 345 350
 Phe Asn Lys Gln Phe Gln Tyr Gln Asn Arg Ile Ala Ala Glu Phe Asn
 355 360 365
 Thr Leu Tyr His Trp His Pro Leu Leu Pro Asp Thr Phe Gln Ile His
 370 375 380
 Asp Gln Lys Tyr Asn Tyr Gln Gln Phe Ile Tyr Asn Asn Ser Ile Leu
 385 390 395 400
 Leu Glu His Gly Ile Thr Gln Phe Val Glu Ser Phe Thr Arg Gln Ile
 405 410 415
 Ala Gly Arg Val Ala Gly Gly Arg Asn Val Pro Pro Ala Val Gln Lys
 420 425 430
 Val Ser Gln Ala Ser Ile Asp Gln Ser Arg Gln Met Lys Tyr Gln Ser
 435 440 445
 Phe Asn Glu Tyr Arg Lys Arg Phe Met Leu Lys Pro Tyr Glu Ser Phe
 450 455 460
 Glu Glu Leu Thr Gly Glu Lys Glu Met Ser Ala Glu Leu Glu Ala Leu
 465 470 475 480
 Tyr Gly Asp Ile Asp Ala Val Glu Leu Tyr Pro Ala Leu Leu Val Glu
 485 490 495
 Lys Pro Arg Pro Asp Ala Ile Phe Gly Glu Thr Met Val Glu Val Gly
 500 505 510
 Ala Pro Phe Ser Leu Lys Gly Leu Met Gly Asn Val Ile Cys Ser Pro
 515 520 525
 Ala Tyr Trp Lys Pro Ser Thr Phe Gly Gly Glu Val Gly Phe Gln Ile
 530 535 540
 Ile Asn Thr Ala Ser Ile Gln Ser Leu Ile Cys Asn Asn Val Lys Gly
 545 550 555 560
 Cys Pro Phe Thr Ser Phe Ser Val Pro Asp Pro Glu Leu Ile Lys Thr
 565 570 575
 Val Thr Ile Asn Ala Ser Ser Ser Arg Ser Gly Leu Asp Asp Ile Asn
 580 585 590
 Pro Thr Val Leu Leu Lys Glu Arg Ser Thr Glu Leu
 595 600

53/88

<210> 25
 <211> 360
 <212> PRT
 <213> Homo sapiens

<400> 25
 Met Glu Asp Phe Asn Met Glu Ser Asp Ser Phe Glu Asp Phe Trp Lys
 1 5 10 15
 Gly Glu Asp Leu Ser Asn Tyr Ser Tyr Ser Ser Thr Leu Pro Pro Phe
 20 25 30
 Leu Leu Asp Ala Ala Pro Cys Glu Pro Glu Ser Leu Glu Ile Asn Lys
 35 40 45
 Tyr Phe Val Val Ile Ile Tyr Ala Leu Val Phe Leu Leu Ser Leu Leu
 50 55 60
 Gly Asn Ser Leu Val Met Leu Val Ile Leu Tyr Ser Arg Val Gly Arg
 65 70 75 80
 Ser Val Thr Asp Val Tyr Leu Leu Asn Leu Ala Leu Ala Asp Leu Leu
 85 90 95
 Phe Ala Leu Thr Leu Pro Ile Trp Ala Ala Ser Lys Val Asn Gly Trp
 100 105 110
 Ile Phe Gly Thr Phe Leu Cys Lys Val Val Ser Leu Leu Lys Glu Val
 115 120 125
 Asn Phe Tyr Ser Gly Ile Leu Leu Leu Ala Cys Ile Ser Val Asp Arg
 130 135 140
 Tyr Leu Ala Ile Val His Ala Thr Arg Thr Leu Thr Gln Lys Arg Tyr
 145 150 155 160
 Leu Val Lys Phe Ile Cys Leu Ser Ile Trp Gly Leu Ser Leu Leu Leu
 165 170 175
 Ala Leu Pro Val Leu Leu Phe Arg Arg Thr Val Tyr Ser Ser Asn Val
 180 185 190
 Ser Pro Ala Cys Tyr Glu Asp Met Gly Asn Asn Thr Ala Asn Trp Arg
 195 200 205
 Met Leu Leu Arg Ile Leu Pro Gln Ser Phe Gly Phe Ile Val Pro Leu
 210 215 220
 Leu Ile Met Leu Phe Cys Tyr Gly Phe Thr Leu Arg Thr Leu Phe Lys
 225 230 235 240
 Ala His Met Gly Gln Lys His Arg Ala Met Arg Val Ile Phe Ala Val
 245 250 255
 Val Leu Ile Phe Leu Leu Cys Trp Leu Pro Tyr Asn Leu Val Leu Leu
 260 265 270

54/88

Ala Asp Thr Leu Met Arg Thr Gln Val Ile Gln Glu Thr Cys Glu Arg
 275 280 285

Arg Asn His Ile Asp Arg Ala Leu Asp Ala Thr Glu Ile Leu Gly Ile
 290 295 300

Leu His Ser Cys Leu Asn Pro Leu Ile Tyr Ala Phe Ile Gly Gln Lys
 305 310 315 320

Phe Arg His Gly Leu Leu Lys Ile Leu Ala Ile His Gly Leu Ile Ser
 325 330 335

Lys Asp Ser Leu Pro Lys Asp Ser Arg Pro Ser Phe Val Gly Ser Ser
 340 345 350

Ser Gly His Thr Ser Thr Thr Leu
 355 360

<210> 26
 <211> 198
 <212> PRT
 <213> Homo sapiens

<400> 26
 Met Pro Leu Gly Leu Leu Trp Leu Gly Leu Ala Leu Leu Gly Ala Leu
 1 5 10 15

His Ala Gln Ala Gln Asp Ser Thr Ser Asp Leu Ile Pro Ala Pro Pro
 20 25 30

Leu Ser Lys Val Pro Leu Gln Gln Asn Phe Gln Asp Asn Gln Phe Gln
 35 40 45

Gly Lys Trp Tyr Val Val Gly Leu Ala Gly Asn Ala Ile Leu Arg Glu
 50 55 60

Asp Lys Asp Pro Gln Lys Met Tyr Ala Thr Ile Tyr Glu Leu Lys Glu
 65 70 75 80

Asp Lys Ser Tyr Asn Val Thr Ser Val Leu Phe Arg Lys Lys Lys Cys
 85 90 95

Asp Tyr Trp Ile Arg Thr Phe Val Pro Gly Cys Gln Pro Gly Glu Phe
 100 105 110

Thr Leu Gly Asn Ile Lys Ser Tyr Pro Gly Leu Thr Ser Tyr Leu Val
 115 120 125

Arg Val Val Ser Thr Asn Tyr Asn Gln His Ala Met Val Phe Phe Lys
 130 135 140

Lys Val Ser Gln Asn Arg Glu Tyr Phe Lys Ile Thr Leu Tyr Gly Arg
 145 150 155 160

Thr Lys Glu Leu Thr Ser Glu Leu Lys Glu Asn Phe Ile Arg Phe Ser
 165 170 175

55/88

Lys Tyr Leu Gly Leu Pro Glu Asn His Ile Val Phe Pro Val Pro Ile
 180 185 190

Asp Gln Cys Ile Asp Gly
 195

<210> 27
 <211> 122
 <212> PRT
 <213> Homo sapiens

<400> 27
 Met Lys Leu Leu Thr Gly Leu Val Phe Cys Ser Leu Val Leu Gly Val
 1 5 10 15

Ser Ser Arg Ser Phe Phe Ser Phe Leu Gly Glu Ala Phe Asp Gly Ala
 20 25 30

Arg Asp Met Trp Arg Ala Tyr Ser Asp Met Arg Glu Ala Asn Tyr Ile
 35 40 45

Gly Ser Asp Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Lys
 50 55 60

Arg Gly Pro Gly Gly Val Trp Ala Ala Glu Ala Ile Ser Asp Ala Arg
 65 70 75 80

Glu Asn Ile Gln Arg Phe Phe Gly His Gly Ala Glu Asp Ser Leu Ala
 85 90 95

Asp Gln Ala Ala Asn Glu Trp Gly Arg Ser Gly Lys Asp Pro Asn His
 100 105 110

Phe Arg Pro Ala Gly Leu Pro Glu Lys Tyr
 115 120

<210> 28
 <211> 554
 <212> PRT
 <213> Homo sapiens

<400> 28
 Met Thr Ala Pro Gly Ala Ala Gly Arg Cys Pro Pro Thr Thr Trp Leu
 1 5 10 15

Gly Ser Leu Leu Leu Leu Val Cys Leu Leu Ala Ser Arg Ser Ile Thr
 20 25 30

Glu Glu Val Ser Glu Tyr Cys Ser His Met Ile Gly Ser Gly His Leu
 35 40 45

Gln Ser Leu Gln Arg Leu Ile Asp Ser Gln Met Glu Thr Ser Cys Gln
 50 55 60

56/88

Ile Thr Phe Glu Phe Val Asp Gln Glu Gln Leu Lys Asp Pro Val Cys
 65 70 75 80
 Tyr Leu Lys Lys Ala Phe Leu Leu Val Gln Asp Ile Met Glu Asp Thr
 85 90 95
 Met Arg Phe Arg Asp Asn Thr Ala Asn Pro Ile Ala Ile Val Gln Leu
 100 105 110
 Gln Glu Leu Ser Leu Arg Leu Lys Ser Cys Phe Thr Lys Asp Tyr Glu
 115 120 125
 Glu His Asp Lys Ala Cys Val Arg Thr Phe Tyr Glu Thr Pro Leu Gln
 130 135 140
 Leu Leu Glu Lys Val Lys Asn Val Phe Asn Glu Thr Lys Asn Leu Leu
 145 150 155 160
 Asp Lys Asp Trp Asn Ile Phe Ser Lys Asn Cys Asn Asn Ser Phe Ala
 165 170 175
 Glu Cys Ser Ser Gln Asp Val Val Thr Lys Pro Asp Cys Asn Cys Leu
 180 185 190
 Tyr Pro Lys Ala Ile Pro Ser Ser Asp Pro Ala Ser Val Ser Pro His
 195 200 205
 Gln Pro Leu Ala Pro Ser Met Ala Pro Val Ala Gly Leu Thr Trp Glu
 210 215 220
 Asp Ser Glu Gly Thr Glu Gly Ser Ser Leu Leu Pro Gly Glu Gln Pro
 225 230 235 240
 Leu His Thr Val Asp Pro Gly Ser Ala Lys Gln Arg Pro Pro Arg Ser
 245 250 255
 Thr Cys Gln Ser Phe Glu Pro Pro Glu Thr Pro Val Val Lys Asp Ser
 260 265 270
 Thr Ile Gly Gly Ser Pro Gln Pro Arg Pro Ser Val Gly Ala Phe Asn
 275 280 285
 Pro Gly Met Glu Asp Ile Leu Asp Ser Ala Met Gly Thr Asn Trp Val
 290 295 300
 Pro Glu Glu Ala Ser Gly Glu Ala Ser Glu Ile Pro Val Pro Gln Gly
 305 310 315 320
 Thr Glu Leu Ser Pro Ser Arg Pro Gly Gly Gly Ser Met Gln Thr Glu
 325 330 335
 Pro Ala Arg Pro Ser Asn Phe Leu Ser Ala Ser Ser Pro Leu Pro Ala
 340 345 350
 Ser Ala Lys Gly Gln Gln Pro Ala Asp Val Thr Ala Thr Ala Leu Pro
 355 360 365

57/88

Arg Val Gly Pro Val Met Pro Thr Gly Gln Asp Trp Asn His Thr Pro
 370 375 380
 Gln Lys Thr Asp His Pro Ser Ala Leu Leu Arg Asp Pro Pro Glu Pro
 385 390 395 400
 Gly Ser Pro Arg Ile Ser Ser Leu Arg Pro Gln Ala Leu Ser Asn Pro
 405 410 415
 Ser Thr Leu Ser Ala Gln Pro Gln Leu Ser Arg Ser His Ser Ser Gly
 420 425 430
 Ser Val Leu Pro Leu Gly Glu Leu Glu Gly Arg Arg Ser Thr Arg Asp
 435 440 445
 Arg Thr Ser Pro Ala Glu Pro Glu Ala Ala Pro Ala Ser Glu Gly Ala
 450 455 460
 Ala Arg Pro Leu Pro Arg Phe Asn Ser Val Pro Leu Thr Asp Thr Gly
 465 470 475 480
 His Glu Arg Gln Ser Glu Gly Ser Ser Ser Pro Gln Leu Gln Glu Ser
 485 490 495
 Val Phe His Leu Leu Val Pro Ser Val Ile Leu Val Leu Leu Ala Val
 500 505 510
 Gly Gly Leu Leu Phe Tyr Arg Trp Arg Arg Arg Ser His Gln Glu Pro
 515 520 525
 Gln Arg Ala Asp Ser Pro Leu Glu Gln Pro Glu Gly Ser Pro Leu Thr
 530 535 540
 Gln Asp Asp Arg Gln Val Glu Leu Pro Val
 545 550

<210> 29
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 29
 Met Ala Arg Ala Ala Leu Ser Ala Ala Pro Ser Asn Pro Arg Leu Leu
 1 5 10 15
 Arg Val Ala Leu Leu Leu Leu Leu Val Ala Ala Gly Arg Arg Ala
 20 25 30
 Ala Gly Ala Ser Val Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr
 35 40 45
 Leu Gln Gly Ile His Pro Lys Asn Ile Gln Ser Val Asn Val Lys Ser
 50 55 60
 Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn
 65 70 75 80

Gly Arg Lys Ala Cys Leu Asn Pro Ala Ser Pro Ile Val Lys Lys Ile
85 90 95

Ile Glu Lys Met Leu Asn Ser Asp Lys Ser Asn
100 105

```
<210> 30
<211> 106
<212> PRT
<213> Homo sapiens
```

<400> 30
Met Ala His Ala Thr Leu Ser Ala Ala Pro Ser Asn Pro Arg Leu Leu
1 5 10 15

Arg Val Ala Leu Leu Leu Leu Leu Val Gly Ser Arg Arg Ala Ala
20 25 30

Gly Ala Ser Val Val Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr Leu
35 40 45

Gln Gly Ile His Leu Lys Asn Ile Gln Ser Val Asn Val Arg Ser Pro
50 55 60

Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn Gly
65 70 75 80

Lys Lys Ala Cys Leu Asn Pro Ala Ser Pro Met Val Gln Lys Ile Ile
85 90 95

Glu Lys Ile Leu Asn Lys Gly Ser Thr Asn
100 105

```
<210> 31
<211> 300
<212> PRT
<213> Homo sapiens
```

<400> 31
Met Arg Ile Ala Val Ile Cys Phe Cys Leu Leu Gly Ile Thr Cys Ala
1 5 10 15

Ile Pro Val Lys Gln Ala Asp Ser Gly Ser Ser Glu Glu Lys Gln Leu
20 25 30

Tyr Asn Lys Tyr Pro Asp Ala Val Ala Thr Trp Leu Asn Pro Asp Pro
35 40 45

Ser Gln Lys Gln Asn Leu Leu Ala Pro Gln Thr Leu Pro Ser Lys Ser
50 55 60

Asn Glu Ser His Asp His Met Asp Asp Met Asp Asp Glu Asp Asp Asp
65 70 75 80

Asp	His	Val	Asp	Ser	Gln	Asp	Ser	Ile	Asp	Ser	Asn	Asp	Ser	Asp	Asp
				85				90				95			
Val	Asp	Asp	Thr	Asp	Asp	Ser	His	Gln	Ser	Asp	Glu	Ser	His	His	Ser
				100				105				110			
Asp	Glu	Ser	Asp	Glu	Leu	Val	Thr	Asp	Phe	Pro	Thr	Asp	Leu	Pro	Ala
				115				120				125			
Thr	Glu	Val	Phe	Thr	Pro	Val	Val	Pro	Thr	Val	Asp	Thr	Tyr	Asp	Gly
				130				135				140			
Arg	Gly	Asp	Ser	Val	Val	Tyr	Gly	Leu	Arg	Ser	Lys	Ser	Lys	Lys	Phe
145				150				155				160			
Arg	Arg	Pro	Asp	Ile	Gln	Tyr	Pro	Asp	Ala	Thr	Asp	Glu	Asp	Ile	Thr
				165				170				175			
Ser	His	Met	Glu	Ser	Glu	Glu	Leu	Asn	Gly	Ala	Tyr	Lys	Ala	Ile	Pro
				180				185				190			
Val	Ala	Gln	Asp	Leu	Asn	Ala	Pro	Ser	Asp	Trp	Asp	Ser	Arg	Gly	Lys
				195				200				205			
Asp	Ser	Tyr	Glu	Thr	Ser	Gln	Leu	Asp	Asp	Gln	Ser	Ala	Glu	Thr	His
				210				215				220			
Ser	His	Lys	Gln	Ser	Arg	Leu	Tyr	Lys	Arg	Lys	Ala	Asn	Asp	Glu	Ser
225				230				235				240			
Asn	Glu	His	Ser	Asp	Val	Ile	Asp	Ser	Gln	Glu	Leu	Ser	Lys	Val	Ser
				245				250				255			
Arg	Glu	Phe	His	Ser	His	Glu	Phe	His	Ser	His	Glu	Asp	Met	Leu	Val
				260				265				270			
Val	Asp	Pro	Lys	Ser	Lys	Glu	Glu	Asp	Lys	His	Leu	Lys	Phe	Arg	Ile
				275				280				285			
Ser	His	Glu	Leu	Asp	Ser	Ala	Ser	Ser	Glu	Val	Asn				
				290				295				300			

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<400> 32
Met Glu His Gln Leu Leu Cys Cys Glu Val Glu Thr Ile Arg Arg Ala
 1             5             10             15
Tyr Pro Asp Ala Asn Leu Leu Asn Asp Arg Val Leu Arg Ala Met Leu
          20          25          30

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60/88

Lys Ala Glu Glu Thr Cys Ala Pro Ser Val Ser Tyr Phe Lys Cys Val
 35 40 45
 Gln Lys Glu Val Leu Pro Ser Met Arg Lys Ile Val Ala Thr Trp Met
 50 55 60
 Leu Glu Val Cys Glu Glu Gln Lys Cys Glu Glu Glu Val Phe Pro Leu
 65 70 75 80
 Ala Met Asn Tyr Leu Asp Arg Phe Leu Ser Leu Glu Pro Val Lys Lys
 85 90 95
 Ser Arg Leu Gln Leu Leu Gly Ala Thr Cys Met Phe Val Ala Ser Lys
 100 105 110
 Met Lys Glu Thr Ile Pro Leu Thr Ala Glu Lys Leu Cys Ile Tyr Thr
 115 120 125
 Asp Gly Ser Ile Arg Pro Glu Glu Leu Leu Gln Met Glu Leu Leu Leu
 130 135 140
 Val Asn Lys Leu Lys Trp Asn Leu Ala Ala Met Thr Pro His Asp Phe
 145 150 155 160
 Ile Glu His Phe Leu Ser Lys Met Pro Glu Ala Glu Glu Asn Lys Gln
 165 170 175
 Ile Ile Arg Lys His Ala Gln Thr Phe Val Ala Ser Cys Ala Thr Asp
 180 185 190
 Val Lys Phe Ile Ser Asn Pro Pro Ser Met Val Ala Ala Gly Ser Val
 195 200 205
 Val Ala Ala Val Gln Gly Leu Asn Leu Arg Ser Pro Asn Asn Phe Leu
 210 215 220
 Ser Tyr Tyr Arg Leu Thr Arg Phe Leu Ser Arg Val Ile Lys Cys Asp
 225 230 235 240
 Pro Asp Cys Leu Arg Ala Cys Gln Glu Gln Ile Glu Ala Leu Leu Glu
 245 250 255
 Ser Ser Leu Arg Gln Ala Gln Gln Asn Met Asp Pro Lys Ala Ala Glu
 260 265 270
 Glu Glu Glu Glu Glu Glu Glu Glu Val Asp Leu Ala Cys Thr Pro Thr
 275 280 285
 Asp Val Arg Asp Val Asp Ile
 290 295

<210> 33

<211> 439

<212> PRT

<213> Homo sapiens

61/88

<400> 33

```

Met Pro Leu Asn Val Ser Phe Thr Asn Arg Asn Tyr Asp Leu Asp Tyr
 1          5          10          15

Asp Ser Val Gln Pro Tyr Phe Tyr Cys Asp Glu Glu Glu Asn Phe Tyr
          20          25          30

Gln Gln Gln Gln Gln Ser Glu Leu Gln Pro Pro Ala Pro Ser Glu Asp
          35          40          45

Ile Trp Lys Lys Phe Glu Leu Leu Pro Thr Pro Pro Leu Ser Pro Ser
 50          55          60

Arg Arg Ser Gly Leu Cys Ser Pro Ser Tyr Val Ala Val Thr Pro Phe
 65          70          75          80

Ser Leu Arg Gly Asp Asn Asp Gly Gly Gly Gly Ser Phe Ser Thr Ala
          85          90          95

Asp Gln Leu Glu Met Val Thr Glu Leu Leu Gly Gly Asp Met Val Asn
          100          105          110

Gln Ser Phe Ile Cys Asp Pro Asp Asp Glu Thr Phe Ile Lys Asn Ile
          115          120          125

Ile Ile Gln Asp Cys Met Trp Ser Gly Phe Ser Ala Ala Ala Lys Leu
          130          135          140

Val Ser Glu Lys Leu Ala Ser Tyr Gln Ala Ala Arg Lys Asp Ser Gly
          145          150          155          160

Ser Pro Asn Pro Ala Arg Gly His Ser Val Cys Ser Thr Ser Ser Leu
          165          170          175

Tyr Leu Gln Asp Leu Ser Ala Ala Ala Ser Glu Cys Ile Asp Pro Ser
          180          185          190

Val Val Phe Pro Tyr Pro Leu Asn Asp Ser Ser Ser Pro Lys Ser Cys
          195          200          205

Ala Ser Gln Asp Ser Ser Ala Phe Ser Pro Ser Ser Asp Ser Leu Leu
          210          215          220

Ser Ser Thr Glu Ser Ser Pro Gln Gly Ser Pro Glu Pro Leu Val Leu
          225          230          235          240

His Glu Glu Thr Pro Pro Thr Thr Ser Ser Asp Ser Glu Glu Glu Gln
          245          250          255

Glu Asp Glu Glu Glu Ile Asp Val Val Ser Val Glu Lys Arg Gln Ala
          260          265          270

Pro Gly Lys Arg Ser Glu Ser Gly Ser Pro Ser Ala Gly Gly His Ser
          275          280          285

Lys Pro Pro His Ser Pro Leu Val Leu Lys Arg Cys His Val Ser Thr
          290          295          300

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62/88

His Gln His Asn Tyr Ala Ala Pro Pro Ser Thr Arg Lys Asp Tyr Pro
 305 310 315 320
 Ala Ala Lys Arg Val Lys Leu Asp Ser Val Arg Val Leu Arg Gln Ile
 325 330 335
 Ser Asn Asn Arg Lys Cys Thr Ser Pro Arg Ser Ser Asp Thr Glu Glu
 340 345 350
 Asn Val Lys Arg Arg Thr His Asn Val Leu Glu Arg Gln Arg Arg Asn
 355 360 365
 Glu Leu Lys Arg Ser Phe Phe Ala Leu Arg Asp Gln Ile Pro Glu Leu
 370 375 380
 Glu Asn Asn Glu Lys Ala Pro Lys Val Val Ile Leu Lys Lys Ala Thr
 385 390 395 400
 Ala Tyr Ile Leu Ser Val Gln Ala Glu Glu Gln Lys Leu Ile Ser Glu
 405 410 415
 Glu Asp Leu Leu Arg Lys Arg Arg Glu Gln Leu Lys His Lys Leu Glu
 420 425 430
 Gln Leu Arg Asn Ser Cys Ala
 435

<210> 34
 <211> 164
 <212> PRT
 <213> Homo sapiens

<400> 34
 Met Ser Glu Pro Ala Gly Asp Val Arg Gln Asn Pro Cys Gly Ser Lys
 1 5 10 15
 Ala Cys Arg Arg Leu Phe Gly Pro Val Asp Ser Glu Gln Leu Ser Arg
 20 25 30
 Asp Cys Asp Ala Leu Met Ala Gly Cys Ile Gln Glu Ala Arg Glu Arg
 35 40 45
 Trp Asn Phe Asp Phe Val Thr Glu Thr Pro Leu Glu Gly Asp Phe Ala
 50 55 60
 Trp Glu Arg Val Arg Gly Leu Gly Leu Pro Lys Leu Tyr Leu Pro Thr
 65 70 75 80
 Gly Pro Arg Arg Gly Arg Asp Glu Leu Gly Gly Gly Arg Arg Pro Gly
 85 90 95
 Thr Ser Pro Ala Leu Leu Gln Gly Thr Ala Glu Glu Asp His Val Asp
 100 105 110
 Leu Ser Leu Ser Cys Thr Leu Val Pro Arg Ser Gly Glu Gln Ala Glu
 115 120 125

63/88

Gly Ser Pro Gly Gly Pro Gly Asp Ser Gln Gly Arg Lys Arg Arg Gln
 130 135 140

Thr Ser Met Thr Asp Phe Tyr His Ser Lys Arg Arg Leu Ile Phe Ser
 145 150 155 160

Lys Arg Lys Pro

<210> 35
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 35
 Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu Leu His Gly
 1 5 10 15

Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val His
 20 25 30

Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg
 35 40 45

Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val
 50 55 60

Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg
 65 70 75 80

Ala Ala Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg Ile Asp Ala
 85 90 95

Ala Glu Gly Pro Ser Asp Ile Pro Asp
 100 105

<210> 36
 <211> 173
 <212> PRT
 <213> Homo sapiens

<400> 36
 Met Gly Arg Gly Arg Cys Val Gly Pro Ser Leu Gln Leu Arg Gly Gln
 1 5 10 15

Glu Trp Arg Cys Ser Pro Leu Val Pro Lys Gly Gly Ala Ala Ala Ala
 20 25 30

Glu Leu Gly Pro Gly Gly Gly Glu Asn Met Val Arg Arg Phe Leu Val
 35 40 45

Thr Leu Arg Ile Arg Arg Ala Cys Gly Pro Pro Arg Val Arg Val Phe
 50 55 60

64/88

Val Val His Ile Pro Arg Leu Thr Gly Glu Trp Ala Ala Pro Gly Ala
 65 70 75 80
 Pro Ala Ala Val Ala Leu Val Leu Met Leu Leu Arg Ser Gln Arg Leu
 85 90 95
 Gly Gln Gln Pro Leu Pro Arg Arg Pro Gly His Asp Asp Gly Gln Arg
 100 105 110
 Pro Ser Gly Gly Ala Ala Ala Ala Pro Arg Arg Gly Ala Gln Leu Arg
 115 120 125
 Arg Pro Arg His Ser His Pro Thr Arg Ala Arg Arg Cys Pro Gly Gly
 130 135 140
 Leu Pro Gly His Ala Gly Gly Ala Ala Pro Gly Arg Gly Ala Ala Gly
 145 150 155 160
 Arg Ala Arg Cys Leu Gly Pro Ser Ala Arg Gly Pro Gly
 165 170

<210> 37

<211> 468

<212> PRT

<213> Homo sapiens

<400> 37

Met Val Asp Thr Glu Ser Pro Leu Cys Pro Leu Ser Pro Leu Glu Ala
 1 5 10 15
 Gly Asp Leu Glu Ser Pro Leu Ser Glu Glu Phe Leu Gln Glu Met Gly
 20 25 30
 Asn Ile Gln Glu Ile Ser Gln Ser Ile Gly Glu Asp Ser Ser Gly Ser
 35 40 45
 Phe Gly Phe Thr Glu Tyr Gln Tyr Leu Gly Ser Cys Pro Gly Ser Asp
 50 55 60
 Gly Ser Val Ile Thr Asp Thr Leu Ser Pro Ala Ser Ser Pro Ser Ser
 65 70 75 80
 Val Thr Tyr Pro Val Val Pro Gly Ser Val Asp Glu Ser Pro Ser Gly
 85 90 95
 Ala Leu Asn Ile Glu Cys Arg Ile Cys Gly Asp Lys Ala Ser Gly Tyr
 100 105 110
 His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg
 115 120 125
 Thr Ile Arg Leu Lys Leu Val Tyr Asp Lys Cys Asp Arg Ser Cys Lys
 130 135 140
 Ile Gln Lys Lys Asn Arg Asn Lys Cys Gln Tyr Cys Arg Phe His Lys
 145 150 155 160

65/88

Cys Leu Ser Val Gly Met Ser His Asn Ala Ile Arg Phe Gly Arg Met
 165 170 175
 Pro Arg Ser Glu Lys Ala Lys Leu Lys Ala Glu Ile Leu Thr Cys Glu
 180 185 190
 His Asp Ile Glu Asp Ser Glu Thr Ala Asp Leu Lys Ser Leu Ala Lys
 195 200 205
 Arg Ile Tyr Glu Ala Tyr Leu Lys Asn Phe Asn Met Asn Lys Val Lys
 210 215 220
 Ala Arg Val Ile Leu Ser Gly Lys Ala Ser Asn Asn Pro Pro Phe Val
 225 230 235 240
 Ile His Asp Met Glu Thr Leu Cys Met Ala Glu Lys Thr Leu Val Ala
 245 250 255
 Lys Leu Val Ala Asn Gly Ile Gln Asn Lys Glu Ala Glu Val Arg Ile
 260 265 270
 Phe His Cys Cys Gln Cys Thr Ser Val Glu Thr Val Thr Glu Leu Thr
 275 280 285
 Glu Phe Ala Lys Ala Ile Pro Gly Phe Ala Asn Leu Asp Leu Asn Asp
 290 295 300
 Gln Val Thr Leu Leu Lys Tyr Gly Val Tyr Glu Ala Ile Phe Ala Met
 305 310 315 320
 Leu Ser Ser Val Met Asn Lys Asp Gly Met Leu Val Ala Tyr Gly Asn
 325 330 335
 Gly Phe Ile Thr Arg Glu Phe Leu Lys Ser Leu Arg Lys Pro Phe Cys
 340 345 350
 Asp Ile Met Glu Pro Lys Phe Asp Phe Ala Met Lys Phe Asn Ala Leu
 355 360 365
 Glu Leu Asp Asp Ser Asp Ile Ser Leu Phe Val Ala Ala Ile Ile Cys
 370 375 380
 Cys Gly Asp Arg Pro Gly Leu Leu Asn Val Gly His Ile Glu Lys Met
 385 390 395 400
 Gln Glu Gly Ile Val His Val Leu Arg Leu His Leu Gln Ser Asn His
 405 410 415
 Pro Asp Asp Ile Phe Leu Phe Pro Lys Leu Leu Gln Lys Met Ala Asp
 420 425 430
 Leu Arg Gln Leu Val Thr Glu His Ala Gln Leu Val Gln Ile Ile Lys
 435 440 445

66/88

Lys Thr Glu Ser Asp Ala Ala Leu His Pro Leu Leu Gln Glu Ile Tyr
 450 455 460

Arg Asp Met Tyr
 465

<210> 38
 <211> 505
 <212> PRT
 <213> Homo sapiens

<400> 38
 Met Gly Glu Thr Leu Gly Asp Ser Pro Ile Asp Pro Glu Ser Asp Ser
 1 5 10 15

Phe Thr Asp Thr Leu Ser Ala Asn Ile Ser Gln Glu Met Thr Met Val
 20 25 30

Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val
 35 40 45

Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro
 50 55 60

Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp
 65 70 75 80

Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp
 85 90 95

Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser
 100 105 110

Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu
 115 120 125

Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp
 130 135 140

Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys
 145 150 155 160

Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys
 165 170 175

Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr
 180 185 190

Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala Ile
 195 200 205

Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala Glu
 210 215 220

Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg
 225 230 235 240

67/88

Ala	Leu	Ala	Lys	His 245	Leu	Tyr	Asp	Ser	Tyr	Ile	Lys	Ser	Phe	Pro	Leu
Thr	Lys	Ala	Lys	Ala	Arg	Ala	Ile	Leu	Thr	Gly	Lys	Thr	Thr	Asp	Lys
Ser	Pro	Phe	Val	Ile	Tyr	Asp	Met	Asn	Ser	Leu	Met	Met	Gly	Glu	Asp
Lys	Ile	Lys	Phe	Lys	His	Ile	Thr	Pro	Leu	Gln	Glu	Gln	Ser	Lys	Glu
Val	Ala	Ile	Arg	Ile	Phe	Gln	Gly	Cys	Gln	Phe	Arg	Ser	Val	Glu	Ala
Val	Gln	Glu	Ile	Thr	Glu	Tyr	Ala	Lys	Ser	Ile	Pro	Gly	Phe	Val	Asn
Leu	Asp	Leu	Asn	Asp	Gln	Val	Thr	Leu	Leu	Lys	Tyr	Gly	Val	His	Glu
Ile	Ile	Tyr	Thr	Met	Leu	Ala	Ser	Leu	Met	Asn	Lys	Asp	Gly	Val	Leu
Ile	Ser	Glu	Gly	Gln	Gly	Phe	Met	Thr	Arg	Glu	Phe	Leu	Lys	Ser	Leu
Arg	Lys	Pro	Phe	Gly	Asp	Phe	Met	Glu	Pro	Lys	Phe	Glu	Phe	Ala	Val
Lys	Phe	Asn	Ala	Leu	Glu	Leu	Asp	Asp	Ser	Asp	Leu	Ala	Ile	Phe	Ile
Ala	Val	Ile	Ile	Leu	Ser	Gly	Asp	Arg	Pro	Gly	Leu	Leu	Asn	Val	Lys
Pro	Ile	Glu	Asp	Ile	Gln	Asp	Asn	Leu	Leu	Gln	Ala	Leu	Glu	Leu	Gln
Leu	Lys	Leu	Asn	His	Pro	Glu	Ser	Ser	Gln	Leu	Phe	Ala	Lys	Leu	Leu
Gln	Lys	Met	Thr	Asp	Leu	Arg	Gln	Ile	Val	Thr	Glu	His	Val	Gln	Leu
Leu	Gln	Val	Ile	Lys	Lys	Thr	Glu	Thr	Asp	Met	Ser	Leu	His	Pro	Leu
Leu	Gln	Glu	Ile	Tyr	Lys	Asp	Leu	Tyr							

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<210> 39
<211> 441
<212> PRT
<213> Homo sapiens
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68/88

<400> 39

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Met Glu Gln Pro Gln Glu Glu Ala Pro Glu Val Arg Glu Glu Glu Glu
 1              5              10              15

Lys Glu Glu Val Ala Glu Ala Glu Gly Ala Pro Glu Leu Asn Gly Gly
      20              25              30

Pro Gln His Ala Leu Pro Ser Ser Ser Tyr Thr Asp Leu Ser Arg Ser
      35              40              45

Ser Ser Pro Pro Ser Leu Leu Asp Gln Leu Gln Met Gly Cys Asp Gly
      50              55              60

Ala Ser Cys Gly Ser Leu Asn Met Glu Cys Arg Val Cys Gly Asp Lys
      65              70              75              80

Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly
      85              90              95

Phe Phe Arg Arg Thr Ile Arg Met Lys Leu Glu Tyr Glu Lys Cys Glu
      100              105              110

Arg Ser Cys Lys Ile Gln Lys Lys Asn Arg Asn Lys Cys Gln Tyr Cys
      115              120              125

Arg Phe Gln Lys Cys Leu Ala Leu Gly Met Ser His Asn Ala Ile Arg
      130              135              140

Phe Gly Arg Met Pro Glu Ala Glu Lys Arg Lys Leu Val Ala Gly Leu
      145              150              155              160

Thr Ala Asn Glu Gly Ser Gln Tyr Asn Pro Gln Val Ala Asp Leu Lys
      165              170              175

Ala Phe Ser Lys His Ile Tyr Asn Ala Tyr Leu Lys Asn Phe Asn Met
      180              185              190

Thr Lys Lys Lys Ala Arg Ser Ile Leu Thr Gly Lys Ala Ser His Thr
      195              200              205

Ala Pro Phe Val Ile His Asp Ile Glu Thr Leu Trp Gln Ala Glu Lys
      210              215              220

Gly Leu Val Trp Lys Gln Leu Val Asn Gly Leu Pro Pro Tyr Lys Glu
      225              230              235              240

Ile Ser Val His Val Phe Tyr Arg Cys Gln Cys Thr Thr Val Glu Thr
      245              250              255

Val Arg Glu Leu Thr Glu Phe Ala Lys Ser Ile Pro Ser Phe Ser Ser
      260              265              270

Leu Phe Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu
      275              280              285

Ala Ile Phe Ala Met Leu Ala Ser Ile Val Asn Lys Asp Gly Leu Leu
      290              295              300

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69/88

Val Ala Asn Gly Ser Gly Phe Val Thr Arg Glu Phe Leu Arg Ser Leu
 305 310 315 320
 Arg Lys Pro Phe Ser Asp Ile Ile Glu Pro Lys Phe Glu Phe Ala Val
 325 330 335
 Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Leu Phe Ile
 340 345 350
 Ala Ala Ile Ile Leu Cys Gly Asp Arg Pro Gly Leu Met Asn Val Pro
 355 360 365
 Arg Val Glu Ala Ile Gln Asp Thr Ile Leu Arg Ala Leu Glu Phe His
 370 375 380
 Leu Gln Ala Asn His Pro Asp Ala Gln Tyr Leu Phe Pro Lys Leu Leu
 385 390 395 400
 Gln Lys Met Ala Asp Leu Arg Gln Leu Val Thr Glu His Ala Gln Met
 405 410 415
 Met Gln Arg Ile Lys Lys Thr Glu Thr Glu Thr Ser Leu His Pro Leu
 420 425 430
 Leu Gln Glu Ile Tyr Lys Asp Met Tyr
 435 440

<210> 40

<211> 742

<212> PRT

<213> Homo sapiens

<400> 40

Met Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro
 1 5 10 15
 Leu Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly
 20 25 30
 Val Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu
 35 40 45
 Ala Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala
 50 55 60
 Gln Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly
 65 70 75 80
 Phe Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile
 85 90 95
 Cys Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Ser Asn Thr Ser
 100 105 110

70/88

Gln	Tyr	Asp	Thr	Tyr	Cys	Phe	Asn	Ala	Ser	Ala	Pro	Pro	Glu	Glu	Asp	115	120	125
Cys	Thr	Ser	Val	Thr	Asp	Leu	Pro	Asn	Ala	Phe	Asp	Gly	Pro	Ile	Thr	130	135	140
Ile	Thr	Ile	Val	Asn	Arg	Asp	Gly	Thr	Arg	Tyr	Val	Gln	Lys	Gly	Glu	145	150	155
Tyr	Arg	Thr	Asn	Pro	Glu	Asp	Ile	Tyr	Pro	Ser	Asn	Pro	Thr	Asp	Asp	165	170	175
Asp	Val	Ser	Ser	Gly	Ser	Ser	Ser	Glu	Arg	Ser	Ser	Thr	Ser	Gly	Gly	180	185	190
Tyr	Ile	Phe	Tyr	Thr	Phe	Ser	Thr	Val	His	Pro	Ile	Pro	Asp	Glu	Asp	195	200	205
Ser	Pro	Trp	Ile	Thr	Asp	Ser	Thr	Asp	Arg	Ile	Pro	Ala	Thr	Thr	Leu	210	215	220
Met	Ser	Thr	Ser	Ala	Thr	Ala	Thr	Glu	Thr	Ala	Thr	Lys	Arg	Gln	Glu	225	230	235
Thr	Trp	Asp	Trp	Phe	Ser	Trp	Leu	Phe	Leu	Pro	Ser	Glu	Ser	Lys	Asn	245	250	255
His	Leu	His	Thr	Thr	Thr	Gln	Met	Ala	Gly	Thr	Ser	Ser	Asn	Thr	Ile	260	265	270
Ser	Ala	Gly	Trp	Glu	Pro	Asn	Glu	Glu	Asn	Glu	Asp	Glu	Arg	Asp	Arg	275	280	285
His	Leu	Ser	Phe	Ser	Gly	Ser	Gly	Ile	Asp	Asp	Asp	Glu	Asp	Phe	Ile	290	295	300
Ser	Ser	Thr	Ile	Ser	Thr	Thr	Pro	Arg	Ala	Phe	Asp	His	Thr	Lys	Gln	305	310	315
Asn	Gln	Asp	Trp	Thr	Gln	Trp	Asn	Pro	Ser	His	Ser	Asn	Pro	Glu	Val	325	330	335
Leu	Leu	Gln	Thr	Thr	Thr	Arg	Met	Thr	Asp	Val	Asp	Arg	Asn	Gly	Thr	340	345	350
Thr	Ala	Tyr	Glu	Gly	Asn	Trp	Asn	Pro	Glu	Ala	His	Pro	Pro	Leu	Ile	355	360	365
His	His	Glu	His	His	Glu	Glu	Glu	Glu	Thr	Pro	His	Ser	Thr	Ser	Thr	370	375	380
Ile	Gln	Ala	Thr	Pro	Ser	Ser	Thr	Thr	Glu	Glu	Thr	Ala	Thr	Gln	Lys	385	390	395
Glu	Gln	Trp	Phe	Gly	Asn	Arg	Trp	His	Glu	Gly	Tyr	Arg	Gln	Thr	Pro	405	410	415

71/88

Lys	Glu	Asp	Ser	His	Ser	Thr	Thr	Gly	Thr	Ala	Ala	Ala	Ser	Ala	His	420	425	430
Thr	Ser	His	Pro	Met	Gln	Gly	Arg	Thr	Thr	Pro	Ser	Pro	Glu	Asp	Ser	435	440	445
Ser	Trp	Thr	Asp	Phe	Phe	Asn	Pro	Ile	Ser	His	Pro	Met	Gly	Arg	Gly	450	455	460
His	Gln	Ala	Gly	Arg	Arg	Met	Asp	Met	Asp	Ser	Ser	His	Ser	Ile	Thr	465	470	475
Leu	Gln	Pro	Thr	Ala	Asn	Pro	Asn	Thr	Gly	Leu	Val	Glu	Asp	Leu	Asp	485	490	495
Arg	Thr	Gly	Pro	Leu	Ser	Met	Thr	Thr	Gln	Gln	Ser	Asn	Ser	Gln	Ser	500	505	510
Phe	Ser	Thr	Ser	His	Glu	Gly	Leu	Glu	Glu	Asp	Lys	Asp	His	Pro	Thr	515	520	525
Thr	Ser	Thr	Leu	Thr	Ser	Ser	Asn	Arg	Asn	Asp	Val	Thr	Gly	Gly	Arg	530	535	540
Arg	Asp	Pro	Asn	His	Ser	Glu	Gly	Ser	Thr	Thr	Leu	Leu	Glu	Gly	Tyr	545	550	555
Thr	Ser	His	Tyr	Pro	His	Thr	Lys	Glu	Ser	Arg	Thr	Phe	Ile	Pro	Val	565	570	575
Thr	Ser	Ala	Lys	Thr	Gly	Ser	Phe	Gly	Val	Thr	Ala	Val	Thr	Val	Gly	580	585	590
Asp	Ser	Asn	Ser	Asn	Val	Asn	Arg	Ser	Leu	Ser	Gly	Asp	Gln	Asp	Thr	595	600	605
Phe	His	Pro	Ser	Gly	Gly	Ser	His	Thr	Thr	His	Gly	Ser	Glu	Ser	Asp	610	615	620
Gly	His	Ser	His	Gly	Ser	Gln	Glu	Gly	Gly	Ala	Asn	Thr	Thr	Ser	Gly	625	630	635
Pro	Ile	Arg	Thr	Pro	Gln	Ile	Pro	Glu	Trp	Leu	Ile	Ile	Leu	Ala	Ser	645	650	655
Leu	Leu	Ala	Leu	Ala	Leu	Ile	Leu	Ala	Val	Cys	Ile	Ala	Val	Asn	Ser	660	665	670
Arg	Arg	Arg	Cys	Gly	Gln	Lys	Lys	Lys	Leu	Val	Ile	Asn	Ser	Gly	Asn	675	680	685
Gly	Ala	Val	Glu	Asp	Arg	Lys	Pro	Ser	Gly	Leu	Asn	Gly	Glu	Ala	Ser	690	695	700
Lys	Ser	Gln	Glu	Met	Val	His	Leu	Val	Asn	Lys	Glu	Ser	Ser	Glu	Thr	705	710	715

<400>	41															
Met	Leu	Met	Arg	Leu	Val	Leu	Thr	Val	Arg	Ser	Asn	Leu	Ile	Pro	Ser	
1				5					10					15		
Pro	Pro	Thr	Tyr	Asn	Ser	Ala	His	Asp	Tyr	Ile	Ser	Trp	Glu	Ser	Phe	
			20					25					30			
Ser	Asn	Val	Ser	Tyr	Tyr	Thr	Arg	Ile	Leu	Pro	Ser	Val	Pro	Lys	Asp	
		35					40					45				
Cys	Pro	Thr	Pro	Met	Gly	Thr	Lys	Gly	Lys	Lys	Gln	Leu	Pro	Asp	Ala	
	50					55					60					
Gln	Leu	Leu	Ala	Arg	Arg	Phe	Leu	Leu	Arg	Arg	Lys	Phe	Ile	Pro	Asp	
65					70					75					80	
Pro	Gln	Gly	Thr	Asn	Leu	Met	Phe	Ala	Phe	Phe	Ala	Gln	His	Phe	Thr	
				85					90					95		
His	Gln	Phe	Phe	Lys	Thr	Ser	Gly	Lys	Met	Gly	Pro	Gly	Phe	Thr	Lys	
			100					105					110			
Ala	Leu	Gly	His	Gly	Val	Asp	Leu	Gly	His	Ile	Tyr	Gly	Asp	Asn	Leu	
		115					120					125				
Glu	Arg	Gln	Tyr	Gln	Leu	Arg	Leu	Phe	Lys	Asp	Gly	Lys	Leu	Lys	Tyr	
	130					135					140					
Gln	Val	Leu	Asp	Gly	Glu	Met	Tyr	Pro	Pro	Ser	Val	Glu	Glu	Ala	Pro	
145					150					155					160	
Val	Leu	Met	His	Tyr	Pro	Arg	Gly	Ile	Pro	Pro	Gln	Ser	Gln	Met	Ala	
			165						170					175		
Val	Gly	Gln	Glu	Val	Phe	Gly	Leu	Leu	Pro	Gly	Leu	Met	Leu	Tyr	Ala	
			180					185					190			
Thr	Leu	Trp	Leu	Arg	Glu	His	Asn	Arg	Val	Cys	Asp	Leu	Leu	Lys	Ala	
		195					200					205				
Glu	His	Pro	Thr	Trp	Gly	Asp	Glu	Gln	Leu	Phe	Gln	Thr	Thr	Arg	Leu	
	210					215					220					
Ile	Leu	Ile	Gly	Glu	Thr	Ile	Lys	Ile	Val	Ile	Glu	Glu	Tyr	Val	Gln	
225					230					235					240	

73/88

Gln Leu Ser Gly Tyr Phe Leu Gln Leu Lys Phe Asp Pro Glu Leu Leu
 245 250 255
 Phe Gly Val Gln Phe Gln Tyr Arg Asn Arg Ile Ala Met Glu Phe Asn
 260 265 270
 His Leu Tyr His Trp His Pro Leu Met Pro Asp Ser Phe Lys Val Gly
 275 280 285
 Ser Gln Glu Tyr Ser Tyr Glu Gln Phe Leu Phe Asn Thr Ser Met Leu
 290 295 300
 Val Asp Tyr Gly Val Glu Ala Leu Val Asp Ala Phe Ser Arg Gln Ile
 305 310 315 320
 Ala Gly Arg Ile Gly Gly Gly Arg Asn Met Asp His His Ile Leu His
 325 330 335
 Val Ala Val Asp Val Ile Arg Glu Ser Arg Glu Met Arg Leu Gln Pro
 340 345 350
 Phe Asn Glu Tyr Arg Lys Arg Phe Gly Met Lys Pro Tyr Thr Ser Phe
 355 360 365
 Gln Glu Leu Val Gly Glu Lys Glu Met Ala Ala Glu Leu Glu Glu Leu
 370 375 380
 Tyr Gly Asp Ile Asp Ala Leu Glu Phe Tyr Pro Gly Leu Leu Leu Glu
 385 390 395 400
 Lys Cys His Pro Asn Ser Ile Phe Gly Glu Ser Met Ile Glu Ile Gly
 405 410 415
 Ala Pro Phe Ser Leu Lys Gly Leu Leu Gly Asn Pro Ile Cys Ser Pro
 420 425 430
 Glu Tyr Trp Lys Pro Ser Thr Phe Gly Gly Glu Val Gly Phe Asn Ile
 435 440 445
 Val Lys Thr Ala Thr Leu Lys Lys Leu Val Cys Leu Asn Thr Lys Thr
 450 455 460
 Cys Pro Tyr Val Ser Phe Arg Val Pro Asp Ala Ser Gln Asp Asp Gly
 465 470 475 480
 Pro Ala Val Glu Arg Pro Ser Thr Glu
 485

<210> 42

<211> 96

<212> PRT

<213> Homo sapiens

<400> 42

Met Ser Glu Ser Ser Ser Lys Ser Ser Gln Pro Leu Ala Ser Lys Gln
 1 5 10 15

74/88

Glu Lys Asp Gly Thr Glu Lys Arg Gly Arg Gly Arg Pro Arg Lys Gln
 20 25 30
 Pro Pro Lys Glu Pro Ser Glu Val Pro Thr Pro Lys Arg Pro Arg Gly
 35 40 45
 Arg Pro Lys Gly Ser Lys Asn Lys Gly Ala Ala Lys Thr Arg Lys Thr
 50 55 60
 Thr Thr Thr Pro Gly Arg Lys Pro Arg Gly Arg Pro Lys Lys Leu Glu
 65 70 75 80
 Lys Glu Glu Glu Glu Gly Ile Ser Gln Glu Ser Ser Glu Glu Glu Gln
 85 90 95

<210> 43
 <211> 79
 <212> PRT
 <213> Homo sapiens

<400> 43
 Met Ala His Lys Gln Ile Tyr Tyr Ser Asp Lys Tyr Phe Asp Glu His
 1 5 10 15
 Tyr Glu Tyr Arg His Val Met Leu Pro Arg Glu Leu Ser Lys Gln Val
 20 25 30
 Pro Lys Thr His Leu Met Ser Glu Glu Glu Trp Arg Arg Leu Gly Val
 35 40 45
 Gln Gln Ser Leu Gly Trp Val His Tyr Met Ile His Glu Pro Glu Pro
 50 55 60
 His Ile Leu Leu Phe Arg Arg Pro Leu Pro Lys Asp Gln Gln Lys
 65 70 75

<210> 44
 <211> 885
 <212> PRT
 <213> Homo sapiens

<400> 44
 Met Val Leu Ser Gly Cys Ala Ile Ile Val Arg Gly Gln Pro Arg Gly
 1 5 10 15
 Gly Pro Pro Pro Glu Arg Gln Ile Asn Leu Ser Asn Ile Arg Ala Gly
 20 25 30
 Asn Leu Ala Arg Arg Ala Ala Ala Thr Gln Pro Asp Ala Lys Asp Thr
 35 40 45
 Pro Asp Glu Pro Trp Ala Phe Pro Ala Arg Glu Phe Leu Arg Lys Lys
 50 55 60

75/88

Leu Ile Gly Lys Glu Val Cys Phe Thr Ile Glu Asn Lys Thr Pro Gln
 65 70 75 80
 Gly Arg Glu Tyr Gly Met Ile Tyr Leu Gly Lys Asp Thr Asn Gly Glu
 85 90 95
 Asn Ile Ala Glu Ser Leu Val Ala Glu Gly Leu Ala Thr Arg Arg Glu
 100 105 110
 Gly Met Arg Ala Asn Asn Pro Glu Gln Asn Arg Leu Ser Glu Cys Glu
 115 120 125
 Glu Gln Ala Lys Ala Ala Lys Lys Gly Met Trp Ser Glu Gly Asn Gly
 130 135 140
 Ser His Thr Ile Arg Asp Leu Lys Tyr Thr Ile Glu Asn Pro Arg His
 145 150 155 160
 Phe Val Asp Ser His His Gln Lys Pro Val Asn Ala Ile Ile Glu His
 165 170 175
 Val Arg Asp Gly Ser Val Val Arg Ala Leu Leu Leu Pro Asp Tyr Tyr
 180 185 190
 Leu Val Thr Val Met Leu Ser Gly Ile Lys Cys Pro Thr Phe Arg Arg
 195 200 205
 Glu Ala Asp Gly Ser Glu Thr Pro Glu Pro Phe Ala Ala Glu Ala Lys
 210 215 220
 Phe Phe Thr Glu Ser Arg Leu Leu Gln Arg Asp Val Gln Ile Ile Leu
 225 230 235 240
 Glu Ser Cys His Asn Gln Asn Ile Val Gly Thr Ile Leu His Pro Asn
 245 250 255
 Gly Asn Ile Thr Glu Leu Leu Leu Lys Glu Gly Phe Ala Arg Cys Val
 260 265 270
 Asp Trp Ser Ile Ala Val Tyr Thr Arg Gly Ala Glu Lys Leu Arg Ala
 275 280 285
 Ala Glu Arg Phe Ala Lys Glu Arg Arg Leu Arg Ile Trp Arg Asp Tyr
 290 295 300
 Val Ala Pro Thr Ala Asn Leu Asp Gln Lys Asp Lys Gln Phe Val Ala
 305 310 315 320
 Lys Val Met Gln Val Leu Asn Ala Asp Ala Ile Val Val Lys Leu Asn
 325 330 335
 Ser Gly Asp Tyr Lys Thr Ile His Leu Ser Ser Ile Arg Pro Pro Arg
 340 345 350
 Leu Glu Gly Glu Asn Thr Gln Asp Lys Asn Lys Lys Leu Arg Pro Leu
 355 360 365

76/88

Tyr	Asp	Ile	Pro	Tyr	Met	Phe	Glu	Ala	Arg	Glu	Phe	Leu	Arg	Lys	Lys	370	375	380
Leu	Ile	Gly	Lys	Lys	Val	Asn	Val	Thr	Val	Asp	Tyr	Ile	Arg	Pro	Ala	385	390	395
Ser	Pro	Ala	Thr	Glu	Thr	Val	Pro	Ala	Phe	Ser	Glu	Arg	Thr	Cys	Ala	405	410	415
Thr	Val	Thr	Ile	Gly	Gly	Ile	Asn	Ile	Ala	Glu	Ala	Leu	Val	Ser	Lys	420	425	430
Gly	Leu	Ala	Thr	Val	Ile	Arg	Tyr	Arg	Gln	Asp	Asp	Asp	Gln	Arg	Ser	435	440	445
Ser	His	Tyr	Asp	Glu	Leu	Leu	Ala	Ala	Glu	Ala	Arg	Ala	Ile	Lys	Asn	450	455	460
Gly	Lys	Gly	Leu	His	Ser	Lys	Lys	Glu	Val	Pro	Ile	His	Arg	Val	Ala	465	470	475
Asp	Ile	Ser	Gly	Asp	Thr	Gln	Lys	Ala	Lys	Gln	Phe	Leu	Pro	Phe	Leu	485	490	495
Gln	Arg	Ala	Gly	Arg	Ser	Glu	Ala	Val	Val	Glu	Tyr	Val	Phe	Ser	Gly	500	505	510
Ser	Arg	Leu	Lys	Leu	Tyr	Leu	Pro	Lys	Glu	Thr	Cys	Leu	Ile	Thr	Phe	515	520	525
Leu	Leu	Ala	Gly	Ile	Glu	Cys	Pro	Arg	Gly	Ala	Arg	Asn	Leu	Pro	Gly	530	535	540
Leu	Val	Gln	Glu	Gly	Glu	Pro	Phe	Ser	Glu	Glu	Ala	Thr	Leu	Phe	Thr	545	550	555
Lys	Glu	Leu	Val	Leu	Gln	Arg	Glu	Val	Glu	Val	Glu	Val	Glu	Ser	Met	565	570	575
Asp	Lys	Ala	Gly	Asn	Phe	Ile	Gly	Trp	Leu	His	Ile	Asp	Gly	Ala	Asn	580	585	590
Leu	Ser	Val	Leu	Leu	Val	Glu	His	Ala	Leu	Ser	Lys	Val	His	Phe	Thr	595	600	605
Ala	Glu	Arg	Ser	Ser	Tyr	Tyr	Lys	Ser	Leu	Leu	Ser	Ala	Glu	Glu	Ala	610	615	620
Ala	Lys	Gln	Lys	Lys	Glu	Lys	Val	Trp	Ala	His	Tyr	Glu	Glu	Gln	Pro	625	630	635
Val	Glu	Glu	Val	Met	Pro	Val	Leu	Glu	Glu	Lys	Glu	Arg	Ser	Ala	Ser	645	650	655
Tyr	Lys	Pro	Val	Phe	Val	Thr	Glu	Ile	Thr	Asp	Asp	Leu	His	Phe	Tyr	660	665	670

77/88

Val	Gln	Asp	Val	Glu	Thr	Gly	Thr	Gln	Phe	Gln	Lys	Leu	Met	Glu	Asn
		675					680					685			
Met	Arg	Asn	Asp	Ile	Ala	Ser	His	Pro	Pro	Val	Glu	Gly	Ser	Tyr	Ala
	690					695					700				
Pro	Arg	Arg	Gly	Glu	Phe	Cys	Ile	Ala	Lys	Phe	Val	Asp	Gly	Glu	Trp
705					710					715					720
Tyr	Arg	Ala	Arg	Val	Glu	Lys	Val	Glu	Ser	Pro	Ala	Lys	Ile	His	Val
				725					730					735	
Phe	Tyr	Ile	Asp	Tyr	Gly	Asn	Arg	Glu	Val	Leu	Pro	Ser	Thr	Arg	Leu
			740					745					750		
Gly	Thr	Leu	Ser	Pro	Ala	Phe	Ser	Thr	Arg	Val	Leu	Pro	Ala	Gln	Ala
		755					760					765			
Thr	Glu	Tyr	Ala	Phe	Ala	Phe	Ile	Gln	Val	Pro	Gln	Asp	Asp	Asp	Ala
	770					775					780				
Arg	Thr	Asp	Ala	Val	Asp	Ser	Val	Val	Arg	Asp	Ile	Gln	Asn	Thr	Gln
785					790					795					800
Cys	Leu	Leu	Asn	Val	Glu	His	Leu	Ser	Ala	Gly	Cys	Pro	His	Val	Thr
			805						810					815	
Leu	Gln	Phe	Ala	Asp	Ser	Lys	Gly	Asp	Val	Gly	Leu	Gly	Leu	Val	Lys
			820					825					830		
Glu	Gly	Leu	Val	Met	Val	Glu	Val	Arg	Lys	Glu	Lys	Gln	Phe	Gln	Lys
		835					840					845			
Val	Ile	Thr	Glu	Tyr	Leu	Asn	Ala	Gln	Glu	Ser	Ala	Lys	Ser	Ala	Arg
	850					855					860				
Leu	Asn	Leu	Trp	Arg	Tyr	Gly	Asp	Phe	Arg	Ala	Asp	Asp	Ala	Asp	Glu
865					870					875					880
Phe	Gly	Tyr	Ser	Arg											
				885											

<210> 45

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 45

agatattgca cgggagaata tacaaa

78/88

<210> 46
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 46
tcaattcctg aaattaaagt tcggata 27

<210> 47
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 47
tctgcagagt tggaagcact cta 23

<210> 48
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 48
gccgaggctt ttctaccaga a 21

<210> 49
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 49
catggcttga tcagcaagga 20

79/88

<210> 50
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 50
tggaagtgtg ccctgaagaa g 21

<210> 51
<211> 23
<212> DNA
<213> Homo sapiens

<400> 51
caaggagctg acttcggaac taa 23

<210> 52
<211> 22
<212> DNA
<213> Homo sapiens

<400> 52
aggaagacg atgtggtttt ca 22

<210> 53
<211> 22
<212> DNA
<213> Homo sapiens

<400> 53
gggacatgtg gagagcctac tc 22

<210> 54
<211> 21
<212> DNA
<213> Homo sapiens

<400> 54
catcatagtt ccccgagca t 21

<210> 55
<211> 21
<212> DNA
<213> Artificial Sequence

80/88

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 55

aagcagcacc agcaagtgaa g

21

<210> 56

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 56

tcatggcctg tgtcagtcaa a

21

<210> 57

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 57

acatgccagc cactgtgata ga

22

<210> 58

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 58

ccctgccttc acaatgatct c

21

<210> 59

<211> 23

<212> DNA

<213> Artificial Sequence

81/88

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 59

ggaattcacc tcaagaacat cca

23

<210> 60

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 60

agtgtggcta tgacttcggt ttg

23

<210> 61

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 61

cagccacaag cagtccagat ta

22

<210> 62

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 62

cctgactatc aatcacatcg gaat

24

<210> 63

<211> 21

<212> DNA

<213> Artificial Sequence

82/88

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 63

ccaggtgctc cacatgacag t

21

<210> 64

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 64

aaacaaccaa caacaaggag aatg

24

<210> 65

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 65

cgtctccaca catcagcaca a

21

<210> 66

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 66

tcttggcagc aggatagtc tt

22

<210> 67

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

83/88

<400> 67
gcagaccagc atgacagatt tc 22

<210> 68
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 68
gcggattagg gcttcctctt 20

<210> 69
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 69
ggcaccagag gcagtaacca t 21

<210> 70
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 70
agcctctctg gttctttcaa tcg 23

<210> 71
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

84/88

<400> 71
tggttcacat cccgcggct

19

<210> 72
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 72
tggctcctca gtagcatcag

20

<210> 73
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 73
tgaagttcaa tgcactggaa ctg

23

<210> 74
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 74
caggacgatc tccacagcaa

20

<210> 75
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 75
tggagtccac gagatcattt aca

23

85/88

<210> 76
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 76
agccttggcc ctcgatat

19

<210> 77
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 77
cactgagttc gccaaagagca t

21

<210> 78
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 78
cacgccatac ttgagaaggg taa

23

<210> 79
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 79
gctagtgatc aacagtggca atg

23

86/88

<210> 80
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 80
gctggcctct ccgttgag

18

<210> 81
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 81
tggtcgggtg ccagttccaa ta

22

<210> 82
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 82
tgccagtggg agagatgggt ga

22

<210> 83
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 83
acaactccag gaaggaaacc aa

22

<210> 84
<211> 19
<212> DNA
<213> Artificial Sequence

87/88

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 84

cgaggactcc tgcgagatg

19

<210> 85

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 85

tgaagaggag tggaggagac ttg

23

<210> 86

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 86

gaatatgtgg ttctggctca tgaa

24

<210> 87

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 87

gagaaggagc gatctgctag ct

22

<210> 88

<211> 23

<212> DNA

<213> Artificial Sequence

88/88

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 88

cacgtagaag tgcaggcat cag

23